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10/512109

SEQUENCE LISTING

DT01 Rec'd PCT/PT~ 21 OCT 2004

<110> KIRIN BEER KABUSHIKI KAISHA

<120> POLYPEPTIDE HAVING AN ACTIVITY TO SUPPORT PROLIFERATION OR SURVIVAL OF HEMATOPOIETIC STEM CELL OR HEMATOPOIETIC PROGENITOR CELL, AND DNA CODING FOR THE SAME

<130> 905W010P1572

<150> US 60/376,001

<151> 2002-04-26

<160> 49

<170> PatentIn version 3.0

<210> 1

<211> 343

<212> DNA

<213> Mus musculus

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tgcatgaaa gattggagca aaactacaaa ccacggacct acaaacaata acatttgctt	480
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 Ser Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp
 35 40 45
 gtg ccc cag gca gag atc tcg ggt gag cac ctg cgg atc tgc ccc cag 192
 Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln
 50 55 60
 ggc tac act tgc tgt acc agt gag atg gag gag aat ttg gcc aac cac 240
 Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn His
 65 70 75 80
 agc cga atg gag ctg gag agc gca ctc cat gac agc agc cgc gcc ctg 288
 Ser Arg Met Glu Leu Glu Ser Ala Leu His Asp Ser Ser Arg Ala Leu
 85 90 95
 cag gcc aca ctg gcc acc cag ctg cat ggc atc gat gac cac ttc cag 336
 Gln Ala Thr Leu Ala Thr Gln Leu His Gly Ile Asp Asp His Phe Gln
 100 105 110
 cgc ctg ctg aat gac tcg gag cgc aca ctg cag gag gct ttc cct ggg 384
 Arg Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Glu Ala Phe Pro Gly
 115 120 125
 gcc ttt ggg gac ctg tat acg cag aac act cgt gcc ttc cgg gac cta 432
 Ala Phe Gly Asp Leu Tyr Thr Gln Asn Thr Arg Ala Phe Arg Asp Leu
 130 135 140
 tat gtt gag ctg cgc ctc tac tac cgt ggg gcc aac ctg cac ctt gag 480
 Tyr Val Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu

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Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys				
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cag ctg cac ccc cag ctg ctg cct gat gac tac ctg gac tgc ctg ggc				576
Gln Leu His Pro Gln Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu Gly				
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aag cag gcg gag gca ctg cgg ccg ttt gga gat gcc cct cga gaa ctg				624
Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Asp Ala Pro Arg Glu Leu				
	195	200	205	
cgc ctg cgg gcc acc cgt gcc ttt gtg gct gca cgt tcc ttt gtg cag				672
Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val Gln				
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Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val Pro				
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ctg gcc cca gaa tgt tct cgg gcc atc atg aag ttg gtc tac tgt gct				768
Leu Ala Pro Glu Cys Ser Arg Ala Ile Met Lys Leu Val Tyr Cys Ala				
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cat tgc cgg gga gtc ccg ggc gcc cgg ccc tgc ccc gac tat tgc cga				816
His Cys Arg Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys Arg				
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aat gtg ctc aaa ggc tgc ctt gcc aac cag gcc gac ctg gat gcc gag				864
Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala Glu				
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tgg agg aac ctc ctg gac tcc atg gtg ctc atc act gac aag ttc tgg				912
Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe Trp				
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ggc ccg tcg ggt gcg gag agt gtc att ggc ggt gtg cac gtg tgg ctg				960
Gly Pro Ser Gly Ala Glu Ser Val Ile Gly Gly Val His Val Trp Leu				
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gcg gag gcc atc aac gcc ctc cag gac aac aag gac aca ctc aca gct				1008
Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Lys Asp Thr Leu Thr Ala				
	325	330	335	
aag gtc atc cag gcc tgt gga aac ccc aag gtc aat ccc cac ggc tct				1056
Lys Val Ile Gln Ala Cys Gly Asn Pro Lys Val Asn Pro His Gly Ser				
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Gly Pro Glu Glu Lys Arg Arg Arg Gly Lys Leu Ala Leu Gln Glu Lys				
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ccc tcc aca ggt act ctg gaa aaa ctg gtc tct gag gcc aag gcc cag				1152
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Ser Glu Lys Met Ala Met Ser Pro Ala Ser Asp Asp Arg Cys Trp Asn
                      405                      410                      415
gga att tcc aag ggc cgg tac cta cca gag gtg atg ggt gac ggg ctg      1296
Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly Leu
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gcc aac cag atc aac aac cct gag gtg gaa gtg gac atc acc aag cca      1344
Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys Pro
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gac atg acc atc cgc cag cag att atg cag ctc aag atc atg acc aac      1392
Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr Asn
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Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp Ala
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Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Gly Gly Cys Pro Asp Asp
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Thr Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Ser Arg Thr Pro
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Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys Thr
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Ser Ala Ala Thr Cys Pro Glu Pro His Ser Phe Phe Leu Leu Phe Leu
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<213> Mus musculus

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Gly	Leu	Gly	Val	Ala	Ser	Asp	Val	Val	Arg	Lys	Val	Ala	Gln	Val	Pro	
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His	Cys	Arg	Gly	Val	Pro	Gly	Ala	Arg	Pro	Cys	Pro	Asp	Tyr	Cys	Arg	
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 405 410 415
 Gly Ile Ser Lys Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly Leu
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 Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys Pro
 435 440 445
 Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr Asn
 450 455 460
 Arg Leu Arg Gly Ala Tyr Gly Gly Asn Asp Val Asp Phe Gln Asp Ala
 465 470 475 480
 Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Gly Cys Pro Asp Asp
 485 490 495
 Thr Cys Gly Arg Arg Val Ser Lys Lys Ser Ser Ser Ser Arg Thr Pro
 500 505 510
 Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys Thr
 515 520 525
 Ser Ala Ala Thr Cys Pro Glu Pro His Ser Phe Phe Leu Leu Phe Leu
 530 535 540
 Val Thr Leu Val Leu Ala Ala Ala Arg Pro Arg Trp Arg
 545 550 555

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 <213> Homo sapiens

<220>
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 Met Glu Leu Arg Ala Arg Gly Trp Trp Leu Leu Cys Ala Ala Ala Ala
 1 5 10 15
 ctg gtc gcc tgc gcc cgc ggg gac ccg gcc agc aag agc cgg agc tgc 96
 Leu Val Ala Cys Ala Arg Gly Asp Pro Ala Ser Lys Ser Arg Ser Cys
 20 25 30
 ggc gag gtc cgc cag atc tac gga gcc aag ggc ttc agc ctg agc gac 144
 Gly Glu Val Arg Gln Ile Tyr Gly Ala Lys Gly Phe Ser Leu Ser Asp

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35	40	45	
gtg ccc cag gcg gag atc tcg ggt gag cac ctg cgg atc tgt ccc cag			192
Val Pro Gln Ala Glu Ile Ser Gly Glu His Leu Arg Ile Cys Pro Gln			
50	55	60	
ggc tac acc tgc tgc acc agc gag atg gag gag aac ctg gcc aac cgc			240
Gly Tyr Thr Cys Cys Thr Ser Glu Met Glu Glu Asn Leu Ala Asn Arg			
65	70	75	80
agc cat gcc gag ctg gag acc gcg ctc cgg gac agc agc cgc gtc ctg			288
Ser His Ala Glu Leu Glu Thr Ala Leu Arg Asp Ser Ser Arg Val Leu			
85	90	95	
cag gcc atg ctt gcc acc cag ctg cgc agc ttc gat gac cac ttc cag			336
Gln Ala Met Leu Ala Thr Gln Leu Arg Ser Phe Asp Asp His Phe Gln			
100	105	110	
cac ctg ctg aac gac tcg gag cgg acg ctg cag gcc acc ttc ccc ggc			384
His Leu Leu Asn Asp Ser Glu Arg Thr Leu Gln Ala Thr Phe Pro Gly			
115	120	125	
gcc ttc gga gag ctg tac acg cag aac gcg agg gcc ttc cgg gac ctg			432
Ala Phe Gly Glu Leu Tyr Thr Gln Asn Ala Arg Ala Phe Arg Asp Leu			
130	135	140	
tac tca gag ctg cgc ctg tac tac cgc ggt gcc aac ctg cac ctg gag			480
Tyr Ser Glu Leu Arg Leu Tyr Tyr Arg Gly Ala Asn Leu His Leu Glu			
145	150	155	160
gag acg ctg gcc gag ttc tgg gcc cgc ctg ctc gag cgc ctc ttc aag			528
Glu Thr Leu Ala Glu Phe Trp Ala Arg Leu Leu Glu Arg Leu Phe Lys			
165	170	175	
cag ctg cac ccc cag ctg ctg ctg cct gat gac tac ctg gac tgc ctg			576
Gln Leu His Pro Gln Leu Leu Leu Pro Asp Asp Tyr Leu Asp Cys Leu			
180	185	190	
ggc aag cag gcc gag gcg ctg cgg ccc ttc ggg gag gcc ccg aga gag			624
Gly Lys Gln Ala Glu Ala Leu Arg Pro Phe Gly Glu Ala Pro Arg Glu			
195	200	205	
ctg cgc ctg cgg gcc acc cgt gcc ttc gtg gct gct cgc tcc ttt gtg			672
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val			
210	215	220	
cag ggc ctg ggc gtg gcc agc gac gtg gtc cgg aaa gtg gct cag gtc			720
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val			
225	230	235	240
ccc ctg ggc ccg gag tgc tcg aga gct gtc atg aag ctg gtc tac tgt			768
Pro Leu Gly Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys			
245	250	255	
gct cac tgc ctg gga gtc ccc ggc gcc agg ccc tgc cct gac tat tgc			816
Ala His Cys Leu Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys			
260	265	270	

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cga aat gtg ctc aag ggc tgc ctt gcc aac cag gcc gac ctg gac gcc	864
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala	
275 280 285	
gag tgg agg aac ctc ctg gac tcc atg gtg ctc atc acc gac aag ttc	912
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe	
290 295 300	
tgg ggt aca tcg ggt gtg gag agt gtc atc ggc agc gtg cac acg tgg	960
Trp Gly Thr Ser Gly Val Glu Ser Val Ile Gly Ser Val His Thr Trp	
305 310 315 320	
ctg gcg gag gcc atc aac gcc ctc cag gac aac agg gac acg ctc acg	1008
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Arg Asp Thr Leu Thr	
325 330 335	
gcc aag gtc atc cag ggc tgc ggg aac ccc aag gtc aac ccc cag ggc	1056
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro Gln Gly	
340 345 350	
cct ggg cct gag gag aag cgg cgc cgg ggc aag ctg gcc ccg cgg gag	1104
Pro Gly Pro Glu Glu Lys Arg Arg Arg Gly Lys Leu Ala Pro Arg Glu	
355 360 365	
agg cca cct tca ggc acg ctg gag aag ctg gtc tct gaa gcc aag gcc	1152
Arg Pro Pro Ser Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala	
370 375 380	
cag ctc cgc gac gtc cag gac ttc tgg atc agc ctc cca ggg aca ctg	1200
Gln Leu Arg Asp Val Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu	
385 390 395 400	
tgc agt gag aag atg gcc ctg agc act gcc agt gat gac cgc tgc tgg	1248
Cys Ser Glu Lys Met Ala Leu Ser Thr Ala Ser Asp Asp Arg Cys Trp	
405 410 415	
aac ggg atg gcc aga ggc cgg tac ctc ccc gag gtc atg ggt gac ggc	1296
Asn Gly Met Ala Arg Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly	
420 425 430	
ctg gcc aac cag atc aac aac ccc gag gtg gag gtg gac atc acc aag	1344
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys	
435 440 445	
ccg gac atg acc atc cgg cag cag atc atg cag ctg aag atc atg acc	1392
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr	
450 455 460	
aac cgg ctg cgc agc gcc tac aac ggc aac gac gtg gac ttc cag gac	1440
Asn Arg Leu Arg Ser Ala Tyr Asn Gly Asn Asp Val Asp Phe Gln Asp	
465 470 475 480	
gcc agt gac gac ggc agc ggc tcg ggc agc ggt gat ggc tgt ctg gat	1488
Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Asp Gly Cys Leu Asp	
485 490 495	
gac ctc tgc ggc cgg aag gtc agc agg aag agc tcc agc tcc cgg acg	1536

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Asp	Leu	Cys	Gly	Arg	Lys	Val	Ser	Arg	Lys	Ser	Ser	Ser	Ser	Arg	Thr		
			500					505						510			
ccc	ttg	acc	cat	gcc	ctc	cca	ggc	ctg	tca	gag	cag	gaa	gga	cag	aag	1584	
Pro	Leu	Thr	His	Ala	Leu	Pro	Gly	Leu	Ser	Glu	Gln	Glu	Gly	Gln	Lys		
		515					520					525					
acc	tcg	gct	gcc	agc	tgc	ccc	cag	ccc	ccg	acc	ttc	ctc	ctg	ccc	ctc	1632	
Thr	Ser	Ala	Ala	Ser	Cys	Pro	Gln	Pro	Pro	Thr	Phe	Leu	Leu	Pro	Leu		
		530					535					540					
ctc	ctc	ttc	ctg	gcc	ctt	aca	gta	gcc	agg	ccc	cgg	tgg	cgg	taa		1677	
Leu	Leu	Phe	Leu	Ala	Leu	Thr	Val	Ala	Arg	Pro	Arg	Trp	Arg				
545						550					555						

<210> 11
 <211> 558
 <212> PRT
 <213> Homo sapiens

<400> 11

Met	Glu	Leu	Arg	Ala	Arg	Gly	Trp	Trp	Leu	Leu	Cys	Ala	Ala	Ala	Ala		
1				5					10					15			
Leu	Val	Ala	Cys	Ala	Arg	Gly	Asp	Pro	Ala	Ser	Lys	Ser	Arg	Ser	Cys		
			20					25					30				
Gly	Glu	Val	Arg	Gln	Ile	Tyr	Gly	Ala	Lys	Gly	Phe	Ser	Leu	Ser	Asp		
		35					40					45					
Val	Pro	Gln	Ala	Glu	Ile	Ser	Gly	Glu	His	Leu	Arg	Ile	Cys	Pro	Gln		
		50					55				60						
Gly	Tyr	Thr	Cys	Cys	Thr	Ser	Glu	Met	Glu	Glu	Asn	Leu	Ala	Asn	Arg		
65					70					75				80			
Ser	His	Ala	Glu	Leu	Glu	Thr	Ala	Leu	Arg	Asp	Ser	Ser	Arg	Val	Leu		
			85						90				95				
Gln	Ala	Met	Leu	Ala	Thr	Gln	Leu	Arg	Ser	Phe	Asp	Asp	His	Phe	Gln		
		100						105					110				
His	Leu	Leu	Asn	Asp	Ser	Glu	Arg	Thr	Leu	Gln	Ala	Thr	Phe	Pro	Gly		
		115					120					125					
Ala	Phe	Gly	Glu	Leu	Tyr	Thr	Gln	Asn	Ala	Arg	Ala	Phe	Arg	Asp	Leu		
		130					135				140						
Tyr	Ser	Glu	Leu	Arg	Leu	Tyr	Tyr	Arg	Gly	Ala	Asn	Leu	His	Leu	Glu		
145					150					155				160			
Glu	Thr	Leu	Ala	Glu	Phe	Trp	Ala	Arg	Leu	Leu	Glu	Arg	Leu	Phe	Lys		
			165					170					175				
Gln	Leu	His	Pro	Gln	Leu	Leu	Leu	Pro	Asp	Asp	Tyr	Leu	Asp	Cys	Leu		
			180					185					190				
Gly	Lys	Gln	Ala	Glu	Ala	Leu	Arg	Pro	Phe	Gly	Glu	Ala	Pro	Arg	Glu		

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195	200	205
Leu Arg Leu Arg Ala Thr Arg Ala Phe Val Ala Ala Arg Ser Phe Val		
210	215	220
Gln Gly Leu Gly Val Ala Ser Asp Val Val Arg Lys Val Ala Gln Val		
225	230	235
Pro Leu Gly Pro Glu Cys Ser Arg Ala Val Met Lys Leu Val Tyr Cys		
245	250	255
Ala His Cys Leu Gly Val Pro Gly Ala Arg Pro Cys Pro Asp Tyr Cys		
260	265	270
Arg Asn Val Leu Lys Gly Cys Leu Ala Asn Gln Ala Asp Leu Asp Ala		
275	280	285
Glu Trp Arg Asn Leu Leu Asp Ser Met Val Leu Ile Thr Asp Lys Phe		
290	295	300
Trp Gly Thr Ser Gly Val Glu Ser Val Ile Gly Ser Val His Thr Trp		
305	310	315
Leu Ala Glu Ala Ile Asn Ala Leu Gln Asp Asn Arg Asp Thr Leu Thr		
325	330	335
Ala Lys Val Ile Gln Gly Cys Gly Asn Pro Lys Val Asn Pro Gln Gly		
340	345	350
Pro Gly Pro Glu Glu Lys Arg Arg Gly Lys Leu Ala Pro Arg Glu		
355	360	365
Arg Pro Pro Ser Gly Thr Leu Glu Lys Leu Val Ser Glu Ala Lys Ala		
370	375	380
Gln Leu Arg Asp Val Gln Asp Phe Trp Ile Ser Leu Pro Gly Thr Leu		
385	390	395
Cys Ser Glu Lys Met Ala Leu Ser Thr Ala Ser Asp Asp Arg Cys Trp		
405	410	415
Asn Gly Met Ala Arg Gly Arg Tyr Leu Pro Glu Val Met Gly Asp Gly		
420	425	430
Leu Ala Asn Gln Ile Asn Asn Pro Glu Val Glu Val Asp Ile Thr Lys		
435	440	445
Pro Asp Met Thr Ile Arg Gln Gln Ile Met Gln Leu Lys Ile Met Thr		
450	455	460
Asn Arg Leu Arg Ser Ala Tyr Asn Gly Asn Asp Val Asp Phe Gln Asp		
465	470	475
Ala Ser Asp Asp Gly Ser Gly Ser Gly Ser Gly Asp Gly Cys Leu Asp		
485	490	495
Asp Leu Cys Gly Arg Lys Val Ser Arg Lys Ser Ser Ser Ser Arg Thr		
500	505	510
Pro Leu Thr His Ala Leu Pro Gly Leu Ser Glu Gln Glu Gly Gln Lys		
515	520	525
Thr Ser Ala Ala Ser Cys Pro Gln Pro Pro Thr Phe Leu Leu Pro Leu		
530	535	540

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Leu Leu Phe Leu Ala Leu Thr Val Ala Arg Pro Arg Trp Arg
 545 550 555

<210> 12
 <211> 369
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(366)

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 1 5 10 15
 ctt gga atc tgg gcc cag atc aca cat gca aca gag aca aaa gaa gtc 96
 Leu Gly Ile Trp Ala Gln Ile Thr His Ala Thr Glu Thr Lys Glu Val
 20 25 30
 cag agc agt ctg aag gca cag caa ggg ctt gaa att gaa atg ttt cac 144
 Gln Ser Ser Leu Lys Ala Gln Gln Gly Leu Glu Ile Glu Met Phe His
 35 40 45
 atg ggc ttt caa gac tct tca gat tgc tgc ctg tcc tat aac tca cgg 192
 Met Gly Phe Gln Asp Ser Ser Asp Cys Cys Leu Ser Tyr Asn Ser Arg
 50 55 60
 att cag tgt tca aga ttt ata ggt tat ttt ccc acc agt ggt ggg tgt 240
 Ile Gln Cys Ser Arg Phe Ile Gly Tyr Phe Pro Thr Ser Gly Gly Cys
 65 70 75 80
 acc agg ccg ggc atc atc ttt atc agc aag agg ggg ttc cag gtc tgt 288
 Thr Arg Pro Gly Ile Ile Phe Ile Ser Lys Arg Gly Phe Gln Val Cys
 85 90 95
 gcc aac ccc agt gat cgg aga gtt cag aga tgc att gaa aga ttg gag 336
 Ala Asn Pro Ser Asp Arg Arg Val Gln Arg Cys Ile Glu Arg Leu Glu
 100 105 110
 caa aac tca caa cca cgg acc tac aaa caa taa 369
 Gln Asn Ser Gln Pro Arg Thr Tyr Lys Gln
 115 120

<210> 13
 <211> 122
 <212> PRT
 <213> Mus musculus

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<400> 13

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Met Lys Pro Phe His Thr Ala Leu Ser Phe Leu Ile Leu Thr Thr Ala
1           5           10           15
Leu Gly Ile Trp Ala Gln Ile Thr His Ala Thr Glu Thr Lys Glu Val
           20           25           30
Gln Ser Ser Leu Lys Ala Gln Gln Gly Leu Glu Ile Glu Met Phe His
           35           40           45
Met Gly Phe Gln Asp Ser Ser Asp Cys Cys Leu Ser Tyr Asn Ser Arg
           50           55           60
Ile Gln Cys Ser Arg Phe Ile Gly Tyr Phe Pro Thr Ser Gly Gly Cys
65           70           75           80
Thr Arg Pro Gly Ile Ile Phe Ile Ser Lys Arg Gly Phe Gln Val Cys
           85           90           95
Ala Asn Pro Ser Asp Arg Arg Val Gln Arg Cys Ile Glu Arg Leu Glu
           100          105          110
Gln Asn Ser Gln Pro Arg Thr Tyr Lys Gln
           115          120

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<210> 14

<211> 1223

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (84)..(1121)

<400> 14

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agtaaaccgg tgtatcgccc acc atg ttg gct gca agg ctt gtg tgt ctc cgg      113
                               Met Leu Ala Ala Arg Leu Val Cys Leu Arg
                               1           5           10
aca cta cct tcc agg gtt ttc cag ccc act ttc atc acc aag gcc tct      161
Thr Leu Pro Ser Arg Val Phe Gln Pro Thr Phe Ile Thr Lys Ala Ser
           15           20           25
cca ctt gtg aag aat tcc atc aca aag aac caa tgg ctc gta aca ccc      209
Pro Leu Val Lys Asn Ser Ile Thr Lys Asn Gln Trp Leu Val Thr Pro
           30           35           40
agc agg gaa tat gct acc aag aca aga att agg act cac cgt ggg aaa      257
Ser Arg Glu Tyr Ala Thr Lys Thr Arg Ile Arg Thr His Arg Gly Lys
           45           50           55
act gga caa gaa ctg aaa gag gca gcc ttg gaa cca tca atg gaa aaa      305
Thr Gly Gln Glu Leu Lys Glu Ala Ala Leu Glu Pro Ser Met Glu Lys

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60	65	70	
atc ttt aaa atc gat caa atg gga agg tgg ttt gtt gct gga gga gca			353
Ile Phe Lys Ile Asp Gln Met Gly Arg Trp Phe Val Ala Gly Gly Ala			
75	80	85	90
gct gtt ggt ctt gga gcg ctc tgc tac tat ggc ttg gga atg tct aat			401
Ala Val Gly Leu Gly Ala Leu Cys Tyr Tyr Gly Leu Gly Met Ser Asn			
	95	100	105
gag att gga gct atc gaa aag gct gta att tgg cct cag tat gta aag			449
Glu Ile Gly Ala Ile Glu Lys Ala Val Ile Trp Pro Gln Tyr Val Lys			
	110	115	120
gat aga att cat tct act tac atg tac tta gca gga agg tat tgt tta			497
Asp Arg Ile His Ser Thr Tyr Met Tyr Leu Ala Gly Arg Tyr Cys Leu			
	125	130	135
aca gct ttg tct gcc ttg gca gta gcc aga aca cct gct ctc atg aac			545
Thr Ala Leu Ser Ala Leu Ala Val Ala Arg Thr Pro Ala Leu Met Asn			
	140	145	150
ttc atg atg aca ggc tct tgg gtg aca att ggt gcg acc ttt gca gcc			593
Phe Met Met Thr Gly Ser Trp Val Thr Ile Gly Ala Thr Phe Ala Ala			
155	160	165	170
atg att gga gct gga atg ctt gta cac tca ata tca tat gag cag agc			641
Met Ile Gly Ala Gly Met Leu Val His Ser Ile Ser Tyr Glu Gln Ser			
	175	180	185
cca ggc cca aag cat ctg gct tgg atg ctg cat tct ggt gtg atg ggt			689
Pro Gly Pro Lys His Leu Ala Trp Met Leu His Ser Gly Val Met Gly			
	190	195	200
gca gtt gtg gct cct ctg acg atc tta ggg ggg cct ctt ctc ctg aga			737
Ala Val Val Ala Pro Leu Thr Ile Leu Gly Gly Pro Leu Leu Leu Arg			
	205	210	215
gcc gca tgg tac acc gct ggt att gtg gga ggc ctc tct act gtg gcc			785
Ala Ala Trp Tyr Thr Ala Gly Ile Val Gly Gly Leu Ser Thr Val Ala			
	220	225	230
atg tgt gcg cct agt gag aag ttt ctg aac atg gga gca ccc ctg gga			833
Met Cys Ala Pro Ser Glu Lys Phe Leu Asn Met Gly Ala Pro Leu Gly			
235	240	245	250
gtg ggc ctg ggt ctt gtc ttt gcg tct tct ctg ggg tct atg ttt ctt			881
Val Gly Leu Gly Leu Val Phe Ala Ser Ser Leu Gly Ser Met Phe Leu			
	255	260	265
ccc cct acc tct gtg gct ggt gcc act ctg tac tca gtg gca atg tat			929
Pro Pro Thr Ser Val Ala Gly Ala Thr Leu Tyr Ser Val Ala Met Tyr			
	270	275	280
ggg gga tta gtt ctt ttc agc atg ttc ctt ctg tat gat act cag aaa			977
Gly Gly Leu Val Leu Phe Ser Met Phe Leu Leu Tyr Asp Thr Gln Lys			
	285	290	295

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gta atc aaa cgt gca gaa ata aca ccc atg tat gga gct caa aag tat 1025
 Val Ile Lys Arg Ala Glu Ile Thr Pro Met Tyr Gly Ala Gln Lys Tyr
 300 305 310
 gat ccc atc aat tcg atg ttg aca atc tac atg gat aca tta aat ata 1073
 Asp Pro Ile Asn Ser Met Leu Thr Ile Tyr Met Asp Thr Leu Asn Ile
 315 320 325 330
 ttt atg cga gtt gca act atg cta gca act gga agc aac aga aag aaa 1121
 Phe Met Arg Val Ala Thr Met Leu Ala Thr Gly Ser Asn Arg Lys Lys
 335 340 345
 tgaagtaacc gcttgtgatg tctccgctca ctgatgtctt gcttggtttaa taggagcaga 1181
 tagtcattac agtttgcacg agcagaattc ccgcgcggcc gc 1223

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 <211> 346
 <212> PRT
 <213> Mus musculus

<400> 15
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 Ile Thr Lys Asn Gln Trp Leu Val Thr Pro Ser Arg Glu Tyr Ala Thr
 35 40 45
 Lys Thr Arg Ile Arg Thr His Arg Gly Lys Thr Gly Gln Glu Leu Lys
 50 55 60
 Glu Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln
 65 70 75 80
 Met Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala
 85 90 95
 Leu Cys Tyr Tyr Gly Leu Gly Met Ser Asn Glu Ile Gly Ala Ile Glu
 100 105 110
 Lys Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr
 115 120 125
 Tyr Met Tyr Leu Ala Gly Arg Tyr Cys Leu Thr Ala Leu Ser Ala Leu
 130 135 140
 Ala Val Ala Arg Thr Pro Ala Leu Met Asn Phe Met Met Thr Gly Ser
 145 150 155 160
 Trp Val Thr Ile Gly Ala Thr Phe Ala Ala Met Ile Gly Ala Gly Met
 165 170 175
 Leu Val His Ser Ile Ser Tyr Glu Gln Ser Pro Gly Pro Lys His Leu
 180 185 190
 Ala Trp Met Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu

18/49

195	200	205
Thr Ile Leu Gly Gly Pro Leu Leu Leu Arg Ala Ala Trp Tyr Thr Ala		
210	215	220
Gly Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu		
225	230	235
Lys Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val		
245	250	255
Phe Ala Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Ser Val Ala		
260	265	270
Gly Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe		
275	280	285
Ser Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu		
290	295	300
Ile Thr Pro Met Tyr Gly Ala Gln Lys Tyr Asp Pro Ile Asn Ser Met		
305	310	315
Leu Thr Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr		
325	330	335
Met Leu Ala Thr Gly Ser Asn Arg Lys Lys		
340	345	

<210> 16
 <211> 1038
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1035)

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ttc cac cca gct ttc acc aag gcc tcc cct gtt gtg aag aat tcc atc	96
Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile	
20 25 30	
acg aag aat caa tgg ctg tta aca cct agc agg gaa tat gcc acc aaa	144
Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys	
35 40 45	
aca aga att ggg atc cgg cgt ggg aga act ggc caa gaa ctc aaa gag	192
Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu	
50 55 60	
gca gca ttg gaa cca tcg atg gaa aaa ata ttt aaa att gat cag atg	240

Ala	Ala	Leu	Glu	Pro	Ser	Met	Glu	Lys	Ile	Phe	Lys	Ile	Asp	Gln	Met	
65					70					75					80	
gga	aga	tgg	ttt	gtt	gct	gga	ggg	gct	gct	gtt	ggt	ctt	gga	gca	ttg	288
Gly	Arg	Trp	Phe	Val	Ala	Gly	Gly	Ala	Ala	Val	Gly	Leu	Gly	Ala	Leu	
				85					90					95		
tgc	tac	tat	ggc	ttg	gga	ctg	tct	aat	gag	att	gga	gct	att	gaa	aag	336
Cys	Tyr	Tyr	Gly	Leu	Gly	Leu	Ser	Asn	Glu	Ile	Gly	Ala	Ile	Glu	Lys	
			100					105					110			
gct	gta	att	tgg	cct	cag	tat	gtc	aag	gat	aga	att	cat	tcc	acc	tat	384
Ala	Val	Ile	Trp	Pro	Gln	Tyr	Val	Lys	Asp	Arg	Ile	His	Ser	Thr	Tyr	
		115					120					125				
atg	tac	tta	gca	ggg	agt	att	ggt	tta	aca	gct	ttg	tct	gcc	ata	gca	432
Met	Tyr	Leu	Ala	Gly	Ser	Ile	Gly	Leu	Thr	Ala	Leu	Ser	Ala	Ile	Ala	
		130					135				140					
atc	agc	aga	acg	cct	gtt	ctc	atg	aac	ttc	atg	atg	aga	ggc	tct	tgg	480
Ile	Ser	Arg	Thr	Pro	Val	Leu	Met	Asn	Phe	Met	Met	Arg	Gly	Ser	Trp	
145				150					155					160		
gtg	aca	att	ggt	gtg	acc	ttt	gca	gcc	atg	gtt	gga	gct	gga	atg	ctg	528
Val	Thr	Ile	Gly	Val	Thr	Phe	Ala	Ala	Met	Val	Gly	Ala	Gly	Met	Leu	
			165					170					175			
gta	cga	tca	ata	cca	tat	gac	cag	agc	cca	ggc	cca	aag	cat	ctt	gct	576
Val	Arg	Ser	Ile	Pro	Tyr	Asp	Gln	Ser	Pro	Gly	Pro	Lys	His	Leu	Ala	
		180					185					190				
tgg	ttg	cta	cat	tct	ggt	gtg	atg	ggt	gca	gtg	gtg	gct	cct	ctg	aca	624
Trp	Leu	Leu	His	Ser	Gly	Val	Met	Gly	Ala	Val	Val	Ala	Pro	Leu	Thr	
		195					200					205				
ata	tta	ggg	ggt	cct	ctt	ctc	atc	aga	gct	gca	tgg	tac	aca	gct	ggc	672
Ile	Leu	Gly	Gly	Pro	Leu	Leu	Ile	Arg	Ala	Ala	Trp	Tyr	Thr	Ala	Gly	
		210					215				220					
att	gtg	gga	ggc	ctc	tcc	act	gtg	gcc	atg	tgt	gcg	ccc	agt	gaa	aag	720
Ile	Val	Gly	Gly	Leu	Ser	Thr	Val	Ala	Met	Cys	Ala	Pro	Ser	Glu	Lys	
225				230					235				240			
ttt	ctg	aac	atg	ggt	gca	ccc	ctg	gga	gtg	ggc	ctg	ggt	ctc	gtc	ttt	768
Phe	Leu	Asn	Met	Gly	Ala	Pro	Leu	Gly	Val	Gly	Leu	Gly	Leu	Val	Phe	
			245					250					255			
gtg	tcc	tca	ttg	gga	tct	atg	ttt	ctt	cca	cct	acc	acc	gtg	gct	ggt	816
Val	Ser	Ser	Leu	Gly	Ser	Met	Phe	Leu	Pro	Pro	Thr	Thr	Val	Ala	Gly	
		260					265					270				
gcc	act	ctt</														

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290	295	300	
tca cca atg tat gga gtt caa aaa tat gat ccc att aac tcg atg ctg			960
Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu			
305	310	315	320
agt atc tac atg gat aca tta aat ata ttt atg cga gtt gca act atg			1008
Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met			
	325	330	335
ctg gca act gga ggc aac aga aag aaa tga			1038
Leu Ala Thr Gly Gly Asn Arg Lys Lys			
	340	345	

<210> 17
 <211> 345
 <212> PRT
 <213> Homo sapiens

<400> 17
 Met Leu Ala Ala Arg Leu Val Cys Leu Arg Thr Leu Pro Ser Arg Val
 1 5 10 15
 Phe His Pro Ala Phe Thr Lys Ala Ser Pro Val Val Lys Asn Ser Ile
 20 25 30
 Thr Lys Asn Gln Trp Leu Leu Thr Pro Ser Arg Glu Tyr Ala Thr Lys
 35 40 45
 Thr Arg Ile Gly Ile Arg Arg Gly Arg Thr Gly Gln Glu Leu Lys Glu
 50 55 60
 Ala Ala Leu Glu Pro Ser Met Glu Lys Ile Phe Lys Ile Asp Gln Met
 65 70 75 80
 Gly Arg Trp Phe Val Ala Gly Gly Ala Ala Val Gly Leu Gly Ala Leu
 85 90 95
 Cys Tyr Tyr Gly Leu Gly Leu Ser Asn Glu Ile Gly Ala Ile Glu Lys
 100 105 110
 Ala Val Ile Trp Pro Gln Tyr Val Lys Asp Arg Ile His Ser Thr Tyr
 115 120 125
 Met Tyr Leu Ala Gly Ser Ile Gly Leu Thr Ala Leu Ser Ala Ile Ala
 130 135 140
 Ile Ser Arg Thr Pro Val Leu Met Asn Phe Met Met Arg Gly Ser Trp
 145 150 155 160
 Val Thr Ile Gly Val Thr Phe Ala Ala Met Val Gly Ala Gly Met Leu
 165 170 175
 Val Arg Ser Ile Pro Tyr Asp Gln Ser Pro Gly Pro Lys His Leu Ala
 180 185 190
 Trp Leu Leu His Ser Gly Val Met Gly Ala Val Val Ala Pro Leu Thr
 195 200 205

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Ile Leu Gly Gly Pro Leu Leu Ile Arg Ala Ala Trp Tyr Thr Ala Gly
 210 215 220
 Ile Val Gly Gly Leu Ser Thr Val Ala Met Cys Ala Pro Ser Glu Lys
 225 230 235 240
 Phe Leu Asn Met Gly Ala Pro Leu Gly Val Gly Leu Gly Leu Val Phe
 245 250 255
 Val Ser Ser Leu Gly Ser Met Phe Leu Pro Pro Thr Thr Val Ala Gly
 260 265 270
 Ala Thr Leu Tyr Ser Val Ala Met Tyr Gly Gly Leu Val Leu Phe Ser
 275 280 285
 Met Phe Leu Leu Tyr Asp Thr Gln Lys Val Ile Lys Arg Ala Glu Val
 290 295 300
 Ser Pro Met Tyr Gly Val Gln Lys Tyr Asp Pro Ile Asn Ser Met Leu
 305 310 315 320
 Ser Ile Tyr Met Asp Thr Leu Asn Ile Phe Met Arg Val Ala Thr Met
 325 330 335
 Leu Ala Thr Gly Gly Asn Arg Lys Lys
 340 345

<210> 18
 <211> 447
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(444)

<400> 18
 atg agc acc tcg tct gcg cgg cct gca gtc ctg gcc ctt gcc ggg ctg 48
 Met Ser Thr Ser Ser Ala Arg Pro Ala Val Leu Ala Leu Ala Gly Leu
 1 5 10 15
 gct ctg ctc ctt ctg ctg tgc ctg ggt cca gat ggc ata agt gga aac 96
 Ala Leu Leu Leu Leu Leu Cys Leu Gly Pro Asp Gly Ile Ser Gly Asn
 20 25 30
 aaa ctc aag aag atg ctc cag aaa cga gaa gga cct gtc ccg tca aag 144
 Lys Leu Lys Lys Met Leu Gln Lys Arg Glu Gly Pro Val Pro Ser Lys
 35 40 45
 act aat gta gct gta gcc gag aac aca gca aag gaa ttc cta ggt ggc 192
 Thr Asn Val Ala Val Ala Glu Asn Thr Ala Lys Glu Phe Leu Gly Gly
 50 55 60
 ctg aag cgt gcc aaa cga cag ctg tgg gac cgt acg cgg cct gag gta 240
 Leu Lys Arg Ala Lys Arg Gln Leu Trp Asp Arg Thr Arg Pro Glu Val

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65	70	75	80	
cag cag tgg tac	cag cag ttc ctc tac	atg ggc ttt gat	gag gct aaa	288
Gln Gln Trp Tyr	Gln Gln Phe Leu Tyr	Met Gly Phe Asp	Glu Ala Lys	
	85	90	95	
ttt gaa gat gat	gtc aac tat tgg cta	aac aga aat cga	aac ggc cat	336
Phe Glu Asp Asp	Val Asn Tyr Trp	Leu Asn Arg Asn	Arg Asn Gly His	
	100	105	110	
gac tac tat ggt	gac tac tac cag	cgt cat tat gat	gaa gat gcg gcc	384
Asp Tyr Tyr Gly	Asp Tyr Tyr Gln	Arg His Tyr Asp	Glu Asp Ala Ala	
	115	120	125	
att ggt ccc cac	agc cgg gaa agc	ttc agg cat gga	gcc agt gtg aac	432
Ile Gly Pro His	Ser Arg Glu Ser	Phe Arg His Gly	Ala Ser Val Asn	
	130	135	140	
tat gat gac tat	taa			447
Tyr Asp Asp Tyr				
145				

<210> 19
 <211> 148
 <212> PRT
 <213> Mus musculus

<400> 19
 Met Ser Thr Ser Ser Ala Arg Pro Ala Val Leu Ala Leu Ala Gly Leu
 1 5 10 15

Ala Leu Leu Leu Leu Leu Cys Leu Gly Pro Asp Gly Ile Ser Gly Asn
 20 25 30

Lys Leu Lys Lys Met Leu Gln Lys Arg Glu Gly Pro Val Pro Ser Lys
 35 40 45

Thr Asn Val Ala Val Ala Glu Asn Thr Ala Lys Glu Phe Leu Gly Gly
 50 55 60

Leu Lys Arg Ala Lys Arg Gln Leu Trp Asp Arg Thr Arg Pro Glu Val
 65 70 75 80

Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met Gly Phe Asp Glu Ala Lys
 85 90 95

Phe Glu Asp Asp Val Asn Tyr Trp Leu Asn Arg Asn Arg Asn Gly His
 100 105 110

Asp Tyr Tyr Gly Asp Tyr Tyr Gln Arg His Tyr Asp Glu Asp Ala Ala
 115 120 125

Ile Gly Pro His Ser Arg Glu Ser Phe Arg His Gly Ala Ser Val Asn
 130 135 140

Tyr Asp Asp Tyr

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145

<210> 20
 <211> 447
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(444)

<400> 20
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 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly Leu
 1 5 10 15
 gcg ctg ctc ctg ctc ctg tgc tgg ggc cca ggt ggc ata agt gga aat 96
 Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser Gly Asn
 20 25 30
 aaa ctc aag ctg atg ctt caa aaa cga gaa gca cct gtt cca act aag 144
 Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val Pro Thr Lys
 35 40 45
 act aaa gtg gcc gtt gat gag aat aaa gcc aaa gaa ttc ctt ggc agc 192
 Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu Phe Leu Gly Ser
 50 55 60
 ctg aag cgc cag aag cgg cag ctg tgg gac cgg act cgg ccc gag gtg 240
 Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg Thr Arg Pro Glu Val
 65 70 75 80
 cag cag tgg tac cag cag ttt ctc tac atg ggc ttt gac gaa gcg aaa 288
 Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met Gly Phe Asp Glu Ala Lys
 85 90 95
 ttt gaa gat gac atc acc tat tgg ctt aac aga gat cga aat gga cat 336
 Phe Glu Asp Asp Ile Thr Tyr Trp Leu Asn Arg Asp Arg Asn Gly His
 100 105 110
 gaa tac tat ggc gat tac tac caa cgt cac tat gat gaa gac tct gca 384
 Glu Tyr Tyr Gly Asp Tyr Tyr Gln Arg His Tyr Asp Glu Asp Ser Ala
 115 120 125
 att ggt ccc cgg agc ccc tac ggc ttt agg cat gga gcc agc gtc aac 432
 Ile Gly Pro Arg Ser Pro Tyr Gly Phe Arg His Gly Ala Ser Val Asn
 130 135 140
 tac gat gac tac taa 447
 Tyr Asp Asp Tyr
 145

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<210> 21
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 21
 Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly Leu
 1 5 10 15
 Ala Leu Leu Leu Leu Leu Cys Trp Gly Pro Gly Gly Ile Ser Gly Asn
 20 25 30
 Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val Pro Thr Lys
 35 40 45
 Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu Phe Leu Gly Ser
 50 55 60
 Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg Thr Arg Pro Glu Val
 65 70 75 80
 Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met Gly Phe Asp Glu Ala Lys
 85 90 95
 Phe Glu Asp Asp Ile Thr Tyr Trp Leu Asn Arg Asp Arg Asn Gly His
 100 105 110
 Glu Tyr Tyr Gly Asp Tyr Tyr Gln Arg His Tyr Asp Glu Asp Ser Ala
 115 120 125
 Ile Gly Pro Arg Ser Pro Tyr Gly Phe Arg His Gly Ala Ser Val Asn
 130 135 140
 Tyr Asp Asp Tyr
 145

<210> 22
 <211> 3132
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (630)..(1358)

<400> 22
 gggggtctgc atctccatcg gaaagtgcgc tggccacatc ccttcggcct ccgggcagtg 60
 ttctgtctcc cttagctcag gcagcgagaa acttcagctg tgaagtgggtg gtggagagag 120
 ccctgggagc agcgactgga cccggacacc aagaagagag tggacgcgcc cctcgactag 180
 gaatcgctct cgcaggcgga gacccagcat ctcagcgctt gcggtcgcgc ttgcccgcc 240
 gcgcgctttt gctaggcgcc gccagccccg aaggaccctc ggggtccgcg gacccttctg 300
 cagccggcgg aatcctaaag ctgccaagag ctcccgccgg gtgtcggcaa actttttccg 360

agcccacgtg	ctgaccaaac	agccccggctc	gcttccagag	cctggcatgg	agcgcgcgc	420
ctaggcacgc	cgtgcagccc	gagagacgcg	agcgcacggt	tcaccgtgga	gggagagatg	480
ctcatcgagc	caaattgatc	attgcagccc	cagggcagtg	acatctgtct	ctgagtcctc	540
cctaggagcg	cgaccgcac	tgtctccttc	caggagcccg	tcatttcctc	gacttttgag	600
aggtgtctct	ccccagcccg	accgtccag	atg cgt ttt	tgc ctc ttc	tca ttt	653
			Met Arg Phe	Cys Leu Phe	Ser Phe	
			1	5		
gcc ctc atc	att ctg aac	tgt atg gat	tac agc cag	tgc caa ggc	aac	701
Ala Leu Ile	Ile Leu Asn	Cys Met Asp	Tyr Ser Gln	Cys Gln Gly	Asn	
10	15	20				
cga tgg aga	cgc aat aag	cga gct agt	tat gta tca	aat ccc att	tgc	749
Arg Trp Arg	Arg Asn Lys	Arg Ala Ser	Tyr Val Ser	Asn Pro Ile	Cys	
25	30	35	40			
aag ggt tgt	ttg tct tgt	tcg aag gac	aat ggt tgc	agc cga tgt	caa	797
Lys Gly Cys	Leu Ser Cys	Ser Lys Asp	Asn Gly Cys	Ser Arg Cys	Gln	
	45	50	55			
cag aag ttg	ttc ttt ttc	ctt cga aga	gaa gga atg	cgt cag tat	gga	845
Gln Lys Leu	Phe Phe Phe	Leu Arg Arg	Glu Gly Met	Arg Gln Tyr	Gly	
	60	65	70			
gag tgc ctg	cat tcc tgc	cca tca ggg	tat tat gga	cac cga gcc	cca	893
Glu Cys Leu	His Ser Cys	Pro Ser Gly	Tyr Tyr Gly	His Arg Ala	Pro	
	75	80	85			
gat atg aac	aga tgt gca	cga tgc aga	ata gaa aac	tgt gat tct	tgc	941
Asp Met Asn	Arg Cys Ala	Arg Cys Arg	Ile Glu Asn	Cys Asp Ser	Cys	
90	95	100				
ttt agc aaa	gac ttt tgt	acg aag tgc	aaa gta ggc	ttt tat ttg	cat	989
Phe Ser Lys	Asp Phe Cys	Thr Lys Cys	Lys Val Gly	Phe Tyr Leu	His	
105	110	115	120			
aga ggc cgc	tgc ttt gat	gaa tgt cca	gat ggt ttt	gca ccg tta	gat	1037
Arg Gly Arg	Cys Phe Asp	Glu Cys Pro	Asp Gly Phe	Ala Pro Leu	Asp	
	125	130	135			
gag act atg	gaa tgt gta	gaa ggt tgt	gaa gtt ggt	cat tgg agc	gaa	1085
Glu Thr Met	Glu Cys Val	Glu Gly Cys	Glu Val Gly	His Trp Ser	Glu	
	140	145	150			
tgg gga acg	tgt agc aga	aac aac cgc	acg tgt gga	ttt aaa tgg	ggt	1133
Trp Gly Thr	Cys Ser Arg	Asn Asn Arg	Thr Cys Gly	Phe Lys Trp	Gly	
	155	160	165			
ctg gaa acc	aga aca cgg	cag att gtt	aaa aag cca	gca aaa gac	aca	1181
Leu Glu Thr	Arg Thr Arg	Gln Ile Val	Lys Lys Pro	Ala Lys Asp	Thr	
	170	175	180			
ata cca tgt	ccg acc att	gcg gag tcc	agg aga tgc	aag atg gcc	atg	1229
Ile Pro Cys	Pro Thr Ile	Ala Glu Ser	Arg Arg Cys	Lys Met Ala	Met	
185	190	195	200			

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agg cac tgt cca gga gga aag aga aca cca aag gca aaa gag aag aga      1277
Arg His Cys Pro Gly Gly Lys Arg Thr Pro Lys Ala Lys Glu Lys Arg
                205                210                215
aac aag aag aag agg cgg aag ctg att gag aga gcc caa gag cag cac      1325
Asn Lys Lys Lys Arg Arg Lys Leu Ile Glu Arg Ala Gln Glu Gln His
                220                225                230
agc gtc ttc ctc gct aca gac aga gtg aac caa taaaatacaa gaaatagctg    1378
Ser Val Phe Leu Ala Thr Asp Arg Val Asn Gln
                235                240
gggcattttg aggttttctg ttttgtttat gttgttgttt tgcaaaagtg cacaaagcta    1438
ctctccagtc cacactgggtg gacagcattc ctgatcctct gaccagtatc cattttcagt    1498
aatgctgcag agggaggtgc ccaagcatgg actcagcggtt atttatgctt tgattggaat    1558
ctggggcctg tgatggcagg agcttgttga gctgagtcag cgggagctga tgcattctgta    1618
ctcttgtgat gagcacagtg tgcataaga acctgtccct ggcacgggtg acccacagga    1678
ggcacaaggc tgtagatcac caccagagaa tgcacctgtg cctattttga tggatggcaa    1738
tgctaaagca gcaagcactg ttcacttgtg actttcattt ctcacactgt gcactgtcaa    1798
agacaaatgt gcatggaaaa atgttttagtg tcacctcatg gcgttctcag catcagtgc    1858
cttcaaacgg tctacaatg agactgtgtt ctactagggg gtatgctgtg gaaattcctg    1918
ctacatttca tcttagtgct aacatgtaca gattctgctg cgctacattc aaagctcatt    1978
actgtatatt tatgctttct ctgtgtaaca agttatacct gataagatgt cactttgttt    2038
ctagtgtatc ttaacatgg tctggtacat ggctattcta gttttggaaa ttaacaagtg    2098
ttttgtgcc tcttgttttc tttgttctc atcatttttg gcgggggttg ggtgggcttg    2158
attctaaccg taagtatagg ataagctagt tttgtatata gagtcaaatg actgatgtca    2218
gaggatcagt gctgatagaa cttcccaggt tcatgtcacg atacacacag agagaaagca    2278
gcatgaggca tcttgccatc agaagccaaa tttcttttga gtcccaaat tgatgactta    2338
tgaaatatag ctgaaaacaa gatttgggtg tagttacttg tatttattat acaatttcca    2398
attacatttt ttttcaaact caaaataacc catgactttg agtgataggt cacttggcaa    2458
tgttcttgaa ttactgggga agctgttgct actaagataa tgagagagaa aatagaatgg    2518
cttcgcccaa gtgagagcca catcttacat ttctctgttg aatcggaatc aactatatta    2578
gaacagaagc ctgatagaag ctttctagtt aacacacaca aggccatggt ttcaaaaaca    2638
tctttgtccc cttaggtcag tttgtcctta gattatgaat tggcaggttc taattgcatt    2698
atttccttgg ctgatccagg aaaaagttag aacaaaataa gttgcatagt tttgaggaaa    2758
catccaaagc aaggcgaagc ctttccttgc cttgcattgg caaaactacc tctttagcat    2818
ttatgttgat tcagaaacat cttgctgata tgtgtagatg ttttaagctt cattgtgaaa    2878
atattgatgc aagataagcc atatatgaat gttgtattca acttttagggc ttgaaattaa    2938
tcctaaagtg ttcacctctc tccatgtcta ttacactct gttcctatct actaagaggg    2998
taggggtctc cttaatatca tacttcattg ttaataagtc aatgcttgtt atgtttcttg    3058
gctgttgttt ttgtgcatta aaaactcaaa attggaaaaa aaaaaaaaaa aaaaaaaaaa    3118
aaaaaaaaaa aaaa

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<210> 23

<211> 243

<212> PRT

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<213> Mus musculus

<400> 23

Met Arg Phe Cys Leu Phe Ser Phe Ala Leu Ile Ile Leu Asn Cys Met
 1 5 10 15
 Asp Tyr Ser Gln Cys Gln Gly Asn Arg Trp Arg Arg Asn Lys Arg Ala
 20 25 30
 Ser Tyr Val Ser Asn Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys
 35 40 45
 Asp Asn Gly Cys Ser Arg Cys Gln Gln Lys Leu Phe Phe Leu Arg
 50 55 60
 Arg Glu Gly Met Arg Gln Tyr Gly Glu Cys Leu His Ser Cys Pro Ser
 65 70 75 80
 Gly Tyr Tyr Gly His Arg Ala Pro Asp Met Asn Arg Cys Ala Arg Cys
 85 90 95
 Arg Ile Glu Asn Cys Asp Ser Cys Phe Ser Lys Asp Phe Cys Thr Lys
 100 105 110
 Cys Lys Val Gly Phe Tyr Leu His Arg Gly Arg Cys Phe Asp Glu Cys
 115 120 125
 Pro Asp Gly Phe Ala Pro Leu Asp Glu Thr Met Glu Cys Val Glu Gly
 130 135 140
 Cys Glu Val Gly His Trp Ser Glu Trp Gly Thr Cys Ser Arg Asn Asn
 145 150 155 160
 Arg Thr Cys Gly Phe Lys Trp Gly Leu Glu Thr Arg Thr Arg Gln Ile
 165 170 175
 Val Lys Lys Pro Ala Lys Asp Thr Ile Pro Cys Pro Thr Ile Ala Glu
 180 185 190
 Ser Arg Arg Cys Lys Met Ala Met Arg His Cys Pro Gly Gly Lys Arg
 195 200 205
 Thr Pro Lys Ala Lys Glu Lys Arg Asn Lys Lys Lys Arg Arg Lys Leu
 210 215 220
 Ile Glu Arg Ala Gln Glu Gln His Ser Val Phe Leu Ala Thr Asp Arg
 225 230 235 240
 Val Asn Gln

<210> 24

<211> 843

<212> DNA

<213> Mus musculus

<220>

<221> CDS

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<222> (132)..(506)

<400> 24

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ggccattatg gccgggggct ttgccgtcc gggagctgac cggccgtgtt cctctctcgt      60
cttctctcgc gccccgcgtc cccgccctcg cgaccccggc tctcctggac tcggcgccgc      120
caacctgggc g atg ccc cgc tac gag ttg gct ttg att ctg aaa gcc atg      170
               Met Pro Arg Tyr Glu Leu Ala Leu Ile Leu Lys Ala Met
                   1             5             10
cgg cgg cca gag acc gct gct gct ttg aaa cgt aca ata gaa tcc ctg      218
Arg Arg Pro Glu Thr Ala Ala Leu Lys Arg Thr Ile Glu Ser Leu
           15             20             25
atg gac cga gga gcc ata gtg agg aac ttg gaa agc ctg ggt gag cgt      266
Met Asp Arg Gly Ala Ile Val Arg Asn Leu Glu Ser Leu Gly Glu Arg
           30             35             40             45
gcg ctc ccc tac agg atc tcg agt cac agc cag cag cac agc cga gga      314
Ala Leu Pro Tyr Arg Ile Ser Ser His Ser Gln Gln His Ser Arg Gly
                   50             55             60
ggg tat ttc ctg gtg gat ttt tat gct ccg aca agt gct gtg gag aac      362
Gly Tyr Phe Leu Val Asp Phe Tyr Ala Pro Thr Ser Ala Val Glu Asn
                   65             70             75
ata ctg gaa cac ttg gcg cga gac att gac gtg gtt aga cca aat att      410
Ile Leu Glu His Leu Ala Arg Asp Ile Asp Val Val Arg Pro Asn Ile
                   80             85             90
gtg aaa cac cct ctg acc cag gaa gta aaa gag tgt gac ggc ata gtc      458
Val Lys His Pro Leu Thr Gln Glu Val Lys Glu Cys Asp Gly Ile Val
                   95             100             105
cca gtc cca ctt gaa gaa aaa ctg tat tca aca aag agg agg aag aag      506
Pro Val Pro Leu Glu Glu Lys Leu Tyr Ser Thr Lys Arg Arg Lys Lys
                   110             115             120             125
tgagaagatt caccagattc tggccttata tttaatccta agggcactat ggggtgctgct      566
aggttggtgt ctaggatact ttagcccatg accattttgc tgcaggaggt agaaactgct      626
ggccgagacc tgccctgatg tctctgctga gatttcatcc cacttgtggg gtttgtcggg      686
agtgggggtg ttcacagtac cactgtagcg tttccaagag caaaatgttt gtcattcaca      746
cttggttgtc ttgcaagcct atatggaaca ctgggagcag agtaataaac atgactttat      806
caacactgga aaaaaaaaaa aaaaaaaaaa aaaaaaa      843

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<210> 25

<211> 125

<212> PRT

<213> Mus musculus

<400> 25

Met Pro Arg Tyr Glu Leu Ala Leu Ile Leu Lys Ala Met Arg Arg Pro

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1	5	10	15
Glu Thr Ala	Ala Leu Lys Arg	Thr Ile Glu Ser	Leu Met Asp Arg
	20	25	30
Gly Ala Ile	Val Arg Asn Leu	Glu Ser Leu Gly	Glu Arg Ala Leu Pro
	35	40	45
Tyr Arg Ile	Ser Ser His Ser	Gln Gln His Ser	Arg Gly Gly Tyr Phe
	50	55	60
Leu Val Asp	Phe Tyr Ala Pro	Thr Ser Ala Val	Glu Asn Ile Leu Glu
65		70	75
His Leu Ala	Arg Asp Ile Asp	Val Val Arg Pro	Asn Ile Val Lys His
	85	90	95
Pro Leu Thr	Gln Glu Val Lys	Glu Cys Asp Gly	Ile Val Pro Val Pro
	100	105	110
Leu Glu Glu	Lys Leu Tyr Ser	Thr Lys Arg Arg	Lys Lys
	115	120	125

<210> 26
 <211> 2490
 <212> DNA
 <213> Mus musculus

<220>
 <221> CDS
 <222> (1)..(2487)

<400> 26	
atg aag ccg ccc ggc agc atc tcc cgg cgg ccg acc ctg acg ggt tgc	48
Met Lys Pro Pro Gly Ser Ile Ser Arg Arg Pro Thr Leu Thr Gly Cys	
1 5 10 15	
agc ctt ccc ggc gcc tcc tgc ggc ccc ggc cgc tgc ccc gcc ggc ccg	96
Ser Leu Pro Gly Ala Ser Cys Gly Pro Gly Arg Cys Pro Ala Gly Pro	
20 25 30	
gtg ccg gcc cgc gcg ccg ccc tgc cgc ctg ctc ctc gtc ctt ctc ctg	144
Val Pro Ala Arg Ala Pro Pro Cys Arg Leu Leu Leu Val Leu Leu Leu	
35 40 45	
cta cct gcg ctc gcc acc tca tcc cgg ccc cgt gcc cgg ggg gcc gct	192
Leu Pro Ala Leu Ala Thr Ser Ser Arg Pro Arg Ala Arg Gly Ala Ala	
50 55 60	
gcg ccc agc gct ccg cac tgg aat gaa act gca gaa aaa acc ctg gga	240
Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu Lys Thr Leu Gly	
65 70 75 80	
gtc ctg gca gat gaa gac aac aca ttg caa caa aat agc agc agc aga	288
Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn Ser Ser Ser Arg	

				85				90				95				
aat	acc	agc	tac	agc	agt	gca	gtg	caa	aaa	gaa	atc	aca	ctg	cct	tca	336
Asn	Thr	Ser	Tyr	Ser	Ser	Ala	Val	Gln	Lys	Glu	Ile	Thr	Leu	Pro	Ser	
100				105				110								
aga	ctg	gtg	tat	tac	atc	aac	cag	gac	tca	gaa	agc	ccc	tat	cat	gtt	384
Arg	Leu	Val	Tyr	Tyr	Ile	Asn	Gln	Asp	Ser	Glu	Ser	Pro	Tyr	His	Val	
115				120				125								
ctt	gac	aca	aag	gcc	aga	cac	caa	cag	aaa	cac	aat	aag	gct	gtg	cat	432
Leu	Asp	Thr	Lys	Ala	Arg	His	Gln	Gln	Lys	His	Asn	Lys	Ala	Val	His	
130				135				140								
ctg	gcc	cag	gca	agc	ttc	cag	atc	gaa	gct	ttc	ggc	tcc	aag	ttc	att	480
Leu	Ala	Gln	Ala	Ser	Phe	Gln	Ile	Glu	Ala	Phe	Gly	Ser	Lys	Phe	Ile	
145				150				155				160				
ctt	gac	ctc	aca	ctg	aac	aat	ggc	ttg	cta	tct	tct	gac	tac	gtg	gag	528
Leu	Asp	Leu	Thr	Leu	Asn	Asn	Gly	Leu	Leu	Ser	Ser	Asp	Tyr	Val	Glu	
165				170				175								
atc	cac	tat	gaa	gac	ggg	aag	cag	atg	tac	tct	aag	ggc	gga	gag	cac	576
Ile	His	Tyr	Glu	Asp	Gly	Lys	Gln	Met	Tyr	Ser	Lys	Gly	Gly	Glu	His	
180				185				190								
tgt	tac	tac	cac	gga	agc	atc	aga	ggc	gtc	aag	gat	tcc	agg	gtg	gct	624
Cys	Tyr	Tyr	His	Gly	Ser	Ile	Arg	Gly	Val	Lys	Asp	Ser	Arg	Val	Ala	
195				200				205								
cta	tcg	acc	tgc	aat	gga	ctc	cat	ggc	atg	ttt	gag	gat	gac	acc	ttt	672
Leu	Ser	Thr	Cys	Asn	Gly	Leu	His	Gly	Met	Phe	Glu	Asp	Asp	Thr	Phe	
210				215				220								
gtg	tat	atg	ata	gag	cct	ctg	gaa	ctg	act	gat	gat	gag	aaa	agc	aca	720
Val	Tyr	Met	Ile	Glu	Pro	Leu	Glu	Leu	Thr	Asp	Asp	Glu	Lys	Ser	Thr	
225				230				235				240				
ggc	cga	ccg	cac	ata	atc	cag	aaa	acc	ttg	gca	gga	cag	tat	tct	aag	768
Gly	Arg	Pro	His	Ile	Ile	Gln	Lys	Thr	Leu	Ala	Gly	Gln	Tyr	Ser	Lys	
245				250				255								
cag	atg	aag	aat	ctc	agc	aca	gat	ggc	agt	gac	cag	tgg	cct	ttg	cta	816
Gln	Met	Lys	Asn	Leu	Ser	Thr	Asp	Gly	Ser	Asp	Gln	Trp	Pro	Leu	Leu	
260				265				270								
cct	gaa	tta	caa	tgg	ctg	aga	aga	agg	aaa	aga	gcg	gtc	aat	cca	tct	864
Pro	Glu	Leu	Gln	Trp	Leu	Arg	Arg	Arg	Lys	Arg	Ala	Val	Asn	Pro	Ser	
275				280				285								
cgt	ggc	gtg	ttt	gaa	gaa	atg	aag	tat	ttg	gag	ctt	atg	att	gtt	aat	912
Arg	Gly	Val	Phe	Glu	Glu	Met	Lys	Tyr	Leu	Glu	Leu	Met	Ile	Val	Asn	
290				295				300								
gat	cac	aag	acg	tat	aag	aag	cac	cgc	tct	tct	cac	gcg	cat	acc	aac	960
Asp	His	Lys	Thr	Tyr	Lys	Lys	His	Arg	Ser	Ser	His	Ala	His	Thr	Asn	
305																

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aac ttc gca aag tct gtg gtc aac ctt gta gat tct att tac aag gaa	1008
Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile Tyr Lys Glu	
325 330 335	
cag ctc aac acc agg gtt gtc ctg gtg gct gtc gag acc tgg acc gag	1056
Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr Trp Thr Glu	
340 345 350	
aag gat cac att gac atc acc atc aac ccc gtg cag atg cta cat gac	1104
Lys Asp His Ile Asp Ile Thr Ile Asn Pro Val Gln Met Leu His Asp	
355 360 365	
ttc tcc aag tac cgg cag cga atc aaa cag cac gct gac gcg gtc cac	1152
Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp Ala Val His	
370 375 380	
ctc atc tcg cgc gtg aca ttc cat tat aag aga agc agt ctg agt tac	1200
Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser Leu Ser Tyr	
385 390 395 400	
ttt gga ggc gtg tgt tct cga ata aga ggg gtt ggt gtg aat gag tat	1248
Phe Gly Gly Val Cys Ser Arg Ile Arg Gly Val Gly Val Asn Glu Tyr	
405 410 415	
ggt ctt cca atg gcg gtg gca caa gta tta tca cag agc ctg gct caa	1296
Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser Leu Ala Gln	
420 425 430	
aac ctt gga atc cag tgg gaa cct tcg agc agg aag cca aaa tgt gaa	1344
Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro Lys Cys Glu	
435 440 445	
tgc ata gag tcc tgg ggc ggc tgc atc atg gaa gaa aca ggg gtg tcc	1392
Cys Ile Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr Gly Val Ser	
450 455 460	
cac tct cga aag ttc tca aag tgc agc att ttg gag tac aga gac ttt	1440
His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr Arg Asp Phe	
465 470 475 480	
tta cag aga ggt ggc gga gca tgt ctt ttc aat agg cca act aag ctg	1488
Leu Gln Arg Gly Gly Gly Ala Cys Leu Phe Asn Arg Pro Thr Lys Leu	
485 490 495	
ttt gag ccc acg gaa tgt gga aat gga tat gtg gag gcc ggg gag gaa	1536
Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala Gly Glu Glu	
500 505 510	
tgc gac tgt ggt ttc cat gtg gaa tgc tat gga gtt tgc tgt aag aag	1584
Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Val Cys Cys Lys Lys	
515 520 525	
tgt tcg ctc tcc aat ggg gcc cac tgc agt gac ggc ccc tgc tgt aac	1632
Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro Cys Cys Asn	
530 535 540	
aac acc tca tgt ctt ttt cag tca cga ggg tat gaa tgt cgg gat gcc	1680

Asn	Thr	Ser	Cys	Leu	Phe	Gln	Ser	Arg	Gly	Tyr	Glu	Cys	Arg	Asp	Ala	
545					550				555						560	
gta	aac	agc	tgt	gat	atc	acc	gag	tac	tgc	act	gga	gac	tct	ggc	cag	1728
Val	Asn	Ser	Cys	Asp	Ile	Thr	Glu	Tyr	Cys	Thr	Gly	Asp	Ser	Gly	Gln	
				565					570						575	
tgc	cca	ccg	aac	ctc	cat	aaa	caa	gat	ggc	tat	agc	tgc	aat	caa	aat	1776
Cys	Pro	Pro	Asn	Leu	His	Lys	Gln	Asp	Gly	Tyr	Ser	Cys	Asn	Gln	Asn	
				580					585						590	
cag	ggt	cgc	tgc	tac	aat	ggc	gag	tgc	aag	aca	agg	gac	aat	caa	tgc	1824
Gln	Gly	Arg	Cys	Tyr	Asn	Gly	Glu	Cys	Lys	Thr	Arg	Asp	Asn	Gln	Cys	
				595					600						605	
cag	tac	atc	tgg	ggg	aca	aag	gct	gcg	ggg	tca	gac	aag	ttc	tgc	tat	1872
Gln	Tyr	Ile	Trp	Gly	Thr	Lys	Ala	Ala	Gly	Ser	Asp	Lys	Phe	Cys	Tyr	
				610					615						620	
gaa	aag	ctg	aac	acg	gaa	ggc	acc	gag	aag	ggc	aat	tgt	gga	aag	gat	1920
Glu	Lys	Leu	Asn	Thr	Glu	Gly	Thr	Glu	Lys	Gly	Asn	Cys	Gly	Lys	Asp	
625					630					635					640	
gga	gac	cgg	tgg	atc	ccg	tgc	agc	aag	cat	gat	gtg	ttc	tgt	gga	ttt	1968
Gly	Asp	Arg	Trp	Ile	Pro	Cys	Ser	Lys	His	Asp	Val	Phe	Cys	Gly	Phe	
				645						650					655	
ctg	ctt	tgc	acc	aat	ctt	acc	cga	gct	cca	cgt	atc	ggt	caa	ctt	caa	2016
Leu	Leu	Cys	Thr	Asn	Leu	Thr	Arg	Ala	Pro	Arg	Ile	Gly	Gln	Leu	Gln	
				660					665						670	
gga	gag	atc	atc	ccg	act	tcc	ttc	tat	cat	caa	ggc	cga	gtg	att	gac	2064
Gly	Glu	Ile	Ile	Pro	Thr	Ser	Phe	Tyr	His	Gln	Gly	Arg	Val	Ile	Asp	
				675					680						685	
tgc	agt	ggt	gct	cat	gta	gtt	tta	gac	gat	gat	aca	gac	gtg	ggt	tac	2112
Cys	Ser	Gly	Ala	His	Val	Val	Leu	Asp	Asp	Asp	Thr	Asp	Val	Gly	Tyr	
				690					695						700	
gtt	gaa	gat	ggg	act	ccg	tgt	ggc	ccc	tcc	atg	atg	tgc	tta	gat	cgg	2160
Val	Glu	Asp	Gly	Thr	Pro	Cys	Gly	Pro	Ser	Met	Met	Cys	Leu	Asp	Arg	
705					710					715					720	
aag	tgc	cta	cag	att	caa	gcc	ctg	aat	atg	agc	agc	tgc	cca	ctt	gac	2208
Lys	Cys	Leu	Gln	Ile	Gln	Ala	Leu	Asn	Met	Ser	Ser	Cys	Pro	Leu	Asp	
				725						730					735	
tca	agg	ggt	aaa	gtc	tgc	tcc	ggc	cac	ggg	gtg	tgt	agc	aac	gaa	gcc	2256
Ser	Arg	Gly	Lys	Val	Cys	Ser	Gly	His	Gly	Val	Cys	Ser	Asn	Glu	Ala	
				740					745						750	
acc	tgc	atc	tgt	gat	ttc	act	tgg	gca	ggc	aca	gac	tgc	agc	atc	cgg	2304
Thr	Cys	Ile	Cys	Asp	Phe	Thr	Trp	Ala	Gly	Thr	Asp	Cys				

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770	775	780	
cct agc gcc acc aat ctc	ata ata ggc tcc atc	gct ggt gcc atc ctg	2400
Pro Ser Ala Thr Asn Leu	Ile Ile Gly Ser Ile Ala	Gly Ala Ile Leu	
785	790	795	800
gta gca gct att gtc ctt	ggg ggc aca ggc tgg	gga ttt aaa aac gtc	2448
Val Ala Ala Ile Val Leu	Gly Gly Thr Gly Trp	Gly Phe Lys Asn Val	
	805	810	815
aag aag agg aga ttc gat	ccc act cag caa ggc	ccc atc tga	2490
Lys Lys Arg Arg Phe Asp	Pro Thr Gln Gln Gly	Pro Ile	
	820	825	

<210> 27
 <211> 829
 <212> PRT
 <213> Mus musculus

<400> 27
 Met Lys Pro Pro Gly Ser Ile Ser Arg Arg Pro Thr Leu Thr Gly Cys
 1 5 10 15
 Ser Leu Pro Gly Ala Ser Cys Gly Pro Gly Arg Cys Pro Ala Gly Pro
 20 25 30

Val Pro Ala Arg Ala Pro Pro Cys Arg Leu Leu Leu Val Leu Leu Leu
 35 40 45
 Leu Pro Ala Leu Ala Thr Ser Ser Arg Pro Arg Ala Arg Gly Ala Ala
 50 55 60
 Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu Lys Thr Leu Gly
 65 70 75 80
 Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn Ser Ser Ser Arg
 85 90 95
 Asn Thr Ser Tyr Ser Ser Ala Val Gln Lys Glu Ile Thr Leu Pro Ser
 100 105 110
 Arg Leu Val Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro Tyr His Val
 115 120 125
 Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys Ala Val His
 130 135 140
 Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser Lys Phe Ile
 145 150 155 160
 Leu Asp Leu Thr Leu Asn Asn Gly Leu Leu Ser Ser Asp Tyr Val Glu
 165 170 175
 Ile His Tyr Glu Asp Gly Lys Gln Met Tyr Ser Lys Gly Gly Glu His
 180 185 190
 Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser Arg Val Ala

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195	200	205
Leu Ser Thr Cys Asn Gly	Leu His Gly Met Phe	Glu Asp Asp Thr Phe
210	215	220
Val Tyr Met Ile Glu Pro	Leu Glu Leu Thr Asp	Asp Glu Lys Ser Thr
225	230	235
Gly Arg Pro His Ile Ile	Gln Lys Thr Leu Ala	Gly Gln Tyr Ser Lys
245	250	255
Gln Met Lys Asn Leu Ser	Thr Asp Gly Ser Asp	Gln Trp Pro Leu Leu
260	265	270
Pro Glu Leu Gln Trp Leu	Arg Arg Arg Lys Arg	Ala Val Asn Pro Ser
275	280	285
Arg Gly Val Phe Glu Glu	Met Lys Tyr Leu Glu	Leu Met Ile Val Asn
290	295	300
Asp His Lys Thr Tyr Lys	Lys His Arg Ser Ser	His Ala His Thr Asn
305	310	315
Asn Phe Ala Lys Ser Val	Val Asn Leu Val Asp	Ser Ile Tyr Lys Glu
325	330	335
Gln Leu Asn Thr Arg Val	Val Leu Val Ala Val	Glu Thr Trp Thr Glu
340	345	350
Lys Asp His Ile Asp Ile	Thr Ile Asn Pro Val	Gln Met Leu His Asp
355	360	365
Phe Ser Lys Tyr Arg Gln	Arg Ile Lys Gln His	Ala Asp Ala Val His
370	375	380
Leu Ile Ser Arg Val Thr	Phe His Tyr Lys Arg	Ser Ser Leu Ser Tyr
385	390	395
Phe Gly Gly Val Cys Ser	Arg Ile Arg Gly Val	Gly Val Asn Glu Tyr
405	410	415
Gly Leu Pro Met Ala Val	Ala Gln Val Leu Ser	Gln Ser Leu Ala Gln
420	425	430
Asn Leu Gly Ile Gln Trp	Glu Pro Ser Ser Arg	Lys Pro Lys Cys Glu
435	440	445
Cys Ile Glu Ser Trp Gly	Gly Cys Ile Met Glu	Glu Thr Gly Val Ser
450	455	460
His Ser Arg Lys Phe Ser	Lys Cys Ser Ile Leu	Glu Tyr Arg Asp Phe
465	470	475
Leu Gln Arg Gly Gly Gly	Ala Cys Leu Phe Asn	Arg Pro Thr Lys Leu
485	490	495
Phe Glu Pro Thr Glu Cys	Gly Asn Gly Tyr Val	Glu Ala Gly Glu Glu
500	505	510
Cys Asp Cys Gly Phe His	Val Glu Cys Tyr Gly	Val Cys Cys Lys Lys
515	520	525
Cys Ser Leu Ser Asn Gly	Ala His Cys Ser Asp	Gly Pro Cys Cys Asn
530	535	540

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Asn	Thr	Ser	Cys	Leu	Phe	Gln	Ser	Arg	Gly	Tyr	Glu	Cys	Arg	Asp	Ala	545	550	555	560
Val	Asn	Ser	Cys	Asp	Ile	Thr	Glu	Tyr	Cys	Thr	Gly	Asp	Ser	Gly	Gln	565	570	575	
Cys	Pro	Pro	Asn	Leu	His	Lys	Gln	Asp	Gly	Tyr	Ser	Cys	Asn	Gln	Asn	580	585	590	
Gln	Gly	Arg	Cys	Tyr	Asn	Gly	Glu	Cys	Lys	Thr	Arg	Asp	Asn	Gln	Cys	595	600	605	
Gln	Tyr	Ile	Trp	Gly	Thr	Lys	Ala	Ala	Gly	Ser	Asp	Lys	Phe	Cys	Tyr	610	615	620	
Glu	Lys	Leu	Asn	Thr	Glu	Gly	Thr	Glu	Lys	Gly	Asn	Cys	Gly	Lys	Asp	625	630	635	640
Gly	Asp	Arg	Trp	Ile	Pro	Cys	Ser	Lys	His	Asp	Val	Phe	Cys	Gly	Phe	645	650	655	
Leu	Leu	Cys	Thr	Asn	Leu	Thr	Arg	Ala	Pro	Arg	Ile	Gly	Gln	Leu	Gln	660	665	670	
Gly	Glu	Ile	Ile	Pro	Thr	Ser	Phe	Tyr	His	Gln	Gly	Arg	Val	Ile	Asp	675	680	685	
Cys	Ser	Gly	Ala	His	Val	Val	Leu	Asp	Asp	Asp	Thr	Asp	Val	Gly	Tyr	690	695	700	
Val	Glu	Asp	Gly	Thr	Pro	Cys	Gly	Pro	Ser	Met	Met	Cys	Leu	Asp	Arg	705	710	715	720
Lys	Cys	Leu	Gln	Ile	Gln	Ala	Leu	Asn	Met	Ser	Ser	Cys	Pro	Leu	Asp	725	730	735	
Ser	Arg	Gly	Lys	Val	Cys	Ser	Gly	His	Gly	Val	Cys	Ser	Asn	Glu	Ala	740	745	750	
Thr	Cys	Ile	Cys	Asp	Phe	Thr	Trp	Ala	Gly	Thr	Asp	Cys	Ser	Ile	Arg	755	760	765	
Asp	Pro	Val	Arg	Asn	Pro	Asn	Pro	Pro	Lys	Asp	Glu	Gly	Pro	Lys	Gly	770	775	780	
Pro	Ser	Ala	Thr	Asn	Leu	Ile	Ile	Gly	Ser	Ile	Ala	Gly	Ala	Ile	Leu	785	790	795	800
Val	Ala	Ala	Ile	Val	Leu	Gly	Gly	Thr	Gly	Trp	Gly	Phe	Lys	Asn	Val	805	810	815	
Lys	Lys	Arg	Arg	Phe	Asp	Pro	Thr	Gln	Gln	Gly	Pro	Ile				820	825		

<210> 28

<211> 2499

<212> DNA

<213> Homo sapiens

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<220>

<221> CDS

<222> (1)..(2496)

<400> 28

atg aag ccg ccc ggc agc agc tcg cgg cag ccg ccc ctg gcg ggc tgc	48
Met Lys Pro Pro Gly Ser Ser Ser Arg Gln Pro Pro Leu Ala Gly Cys	
1 5 10 15	
agc ctt gcc ggc gct tcc tgc ggc ccc caa cgc ggc ccc gcc ggc tcg	96
Ser Leu Ala Gly Ala Ser Cys Gly Pro Gln Arg Gly Pro Ala Gly Ser	
20 25 30	
gtg cct gcc agc gcc ccg gcc cgc acg ccg ccc tgc cgc ctg ctt ctc	144
Val Pro Ala Ser Ala Pro Ala Arg Thr Pro Pro Cys Arg Leu Leu Leu	
35 40 45	
gtc ctt ctc ctg ctg cct ccg ctc gcc gcc tcg tcc cgg ccc cgc gcc	192
Val Leu Leu Leu Leu Pro Pro Leu Ala Ala Ser Ser Arg Pro Arg Ala	
50 55 60	
tgg ggg gct gct gcg ccc agc gct ccg cat tgg aat gaa act gca gaa	240
Trp Gly Ala Ala Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu	
65 70 75 80	
aaa aat ttg gga gtc ctg gca gat gaa gac aat aca ttg caa cag aat	288
Lys Asn Leu Gly Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn	
85 90 95	
agc agc agt aat atc agt tac agc aat gca atg cag aaa gaa atc aca	336
Ser Ser Ser Asn Ile Ser Tyr Ser Asn Ala Met Gln Lys Glu Ile Thr	
100 105 110	
ctg cct tca aga ctc ata tat tac atc aac caa gac tcg gaa agc cct	384
Leu Pro Ser Arg Leu Ile Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro	
115 120 125	
tat cac gtt ctt gac aca aag gca aga cac cag caa aaa cat aat aag	432
Tyr His Val Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys	
130 135 140	
gct gtc cat ctg gcc cag gca agc ttc cag att gaa gcc ttc ggc tcc	480
Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser	
145 150 155 160	
aaa ttc att ctt gac ctc ata ctg aac aat ggt ttg ttg tct tct gat	528
Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly Leu Leu Ser Ser Asp	
165 170 175	
tat gtg gag att cac tac gaa aat ggg aaa cca cag tac tct aag ggt	576
Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro Gln Tyr Ser Lys Gly	
180 185 190	
gga gag cac tgt tac tac cat gga agc atc aga ggc gtc aaa gac tcc	624
Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser	

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195	200	205	
aag gtg gct ctg tca acc tgc aat gga ctt cat ggc atg ttt gaa gat			672
Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp			
210	215	220	
gat acc ttc gtg tat atg ata gag cca cta gag ctg gtt cat gat gag			720
Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu Leu Val His Asp Glu			
225	230	235	240
aaa agc aca ggt cga cca cat ata atc cag aaa acc ttg gca gga cag			768
Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln			
245	250	255	
tat tct aag caa atg aag aat ctc act atg gaa aga ggt gac cag tgg			816
Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu Arg Gly Asp Gln Trp			
260	265	270	
ccc ttt ctc tct gaa tta cag tgg ttg aaa aga agg aag aga gca gtg			864
Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg Arg Lys Arg Ala Val			
275	280	285	
aat cca tca cgt ggt ata ttt gaa gaa atg aaa tat ttg gaa ctt atg			912
Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys Tyr Leu Glu Leu Met			
290	295	300	
att gtt aat gat cac aaa acg tat aag aag cat cgc tct tct cat gca			960
Ile Val Asn Asp His Lys Thr Tyr Lys Lys His Arg Ser Ser His Ala			
305	310	315	320
cat acc aac aac ttt gca aag tcc gtg gtc aac ctt gtg gat tct att			1008
His Thr Asn Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile			
325	330	335	
tac aag gag cag ctc aac acc agg gtt gtc ctg gtg gct gta gag acc			1056
Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr			
340	345	350	
tgg act gag aag gat cag att gac atc acc acc aac cct gtg cag atg			1104
Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met			
355	360	365	
ctc cat gag ttc tca aaa tac cgg cag cgc att aag cag cat gct gat			1152
Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp			
370	375	380	
gct gtg cac ctc atc tcg cgg gtg aca ttt cac tat aag aga agc agt			1200
Ala Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser			
385	390	395	400
ctg agt tac ttt gga ggt gtc tgt tct cgc aca aga gga gtt ggt gtg			1248
Leu Ser Tyr Phe Gly Gly Val Cys Ser Arg Thr Arg Gly Val Gly Val			
405	410	415	
aat gag tat ggt ctt cca atg gca gtg gca caa gta tta tcg cag agc			1296
Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser			
420	425	430	

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ctg gct caa aac ctt gga atc caa tgg gaa cct tct agc aga aag cca	1344
Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro	
435 440 445	
aaa tgt gac tgc aca gaa tcc tgg ggt ggc tgc atc atg gag gaa aca	1392
Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr	
450 455 460	
ggg gtg tcc cat tct cga aaa ttt tca aag tgc agc att ttg gag tat	1440
Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr	
465 470 475 480	
aga gac ttt tta cag aga gga ggt gga gcc tgc ctt ttc aac agg cca	1488
Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala Cys Leu Phe Asn Arg Pro	
485 490 495	
aca aag cta ttt gag ccc acg gaa tgt gga aat gga tac gtg gaa gct	1536
Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala	
500 505 510	
ggg gag gag tgt gat tgt ggt ttt cat gtg gaa tgc tat gga tta tgc	1584
Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Leu Cys	
515 520 525	
tgt aag aaa tgt tcc ctc tcc aac ggg gct cac tgc agc gac ggg ccc	1632
Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro	
530 535 540	
tgc tgt aac aat acc tca tgt ctt ttt cag cca cga ggg tat gaa tgc	1680
Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro Arg Gly Tyr Glu Cys	
545 550 555 560	
cgg gat gct gtg aac gag tgt gat att act gaa tat tgt act gga gac	1728
Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp	
565 570 575	
tct ggt cag tgc cca cca aat ctt cat aag caa gac gga tat gca tgc	1776
Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ala Cys	
580 585 590	
aat caa aat cag ggc cgc tgc tac aat ggc gag tgc aag acc aga gac	1824
Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp	
595 600 605	
aac cag tgt cag tac atc tgg gga aca aag gct gca ggg tct gac aag	1872
Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys	
610 615 620	
ttc tgc tat gaa aag ctg aat aca gaa ggc act gag aag gga aac tgc	1920
Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys	
625 630 635 640	
ggg aag gat gga gac cgg tgg att cag tgc agc aaa cat gat gtg ttc	1968
Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser Lys His Asp Val Phe	
645 650 655	
tgt gga ttc tta ctc tgt acc aat ctt act cga gct cca cgt att ggt	2016

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Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly	
660 665 670	
caa ctt cag ggt gag atc att cca act tcc ttc tac cat caa ggc cgg	2064
Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg	
675 680 685	
gtg att gac tgc agt ggt gcc cat gta gtt tta gat gat gat acg gat	2112
Val Ile Asp Cys Ser Gly Ala His Val Val Leu Asp Asp Asp Thr Asp	
690 695 700	
gtg ggc tat gta gaa gat gga acg cca tgt ggc ccg tct atg atg tgt	2160
Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys	
705 710 715 720	
tta gat cgg aag tgc cta caa att caa gcc cta aat atg agc agc tgt	2208
Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys	
725 730 735	
cca ctc gat tcc aag ggt aaa gtc tgt tgc ggc cat ggg gtg tgt agt	2256
Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly His Gly Val Cys Ser	
740 745 750	
aat gaa gcc acc tgc att tgt gat ttc acc tgg gca ggg aca gat tgc	2304
Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys	
755 760 765	
agt atc cgg gat cca gtt agg aac ctt cac ccc ccc aag gat gaa gga	2352
Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly	
770 775 780	
ccc aag ggt cct agt gcc acc aat ctc ata ata ggc tcc atc gct ggt	2400
Pro Lys Gly Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly	
785 790 795 800	
gcc atc ctg gta gca gct att gtc ctt ggg ggc aca ggc tgg gga ttt	2448
Ala Ile Leu Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe	
805 810 815	
aaa aat gtc aag aag aga agg ttc gat cct act cag caa ggc ccc atc	2496
Lys Asn Val Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile	
820 825 830	
tga	2499

<210> 29
 <211> 832
 <212> PRT
 <213> Homo sapiens

<400> 29
 Met Lys Pro Pro Gly Ser Ser Ser Arg Gln Pro Pro Leu Ala Gly Cys
 1 5 10 15

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Ser Leu Ala Gly Ala Ser Cys Gly Pro Gln Arg Gly Pro Ala Gly Ser
 20 25 30
 Val Pro Ala Ser Ala Pro Ala Arg Thr Pro Pro Cys Arg Leu Leu Leu
 35 40 45
 Val Leu Leu Leu Leu Pro Pro Leu Ala Ala Ser Ser Arg Pro Arg Ala
 50 55 60
 Trp Gly Ala Ala Ala Pro Ser Ala Pro His Trp Asn Glu Thr Ala Glu
 65 70 75 80
 Lys Asn Leu Gly Val Leu Ala Asp Glu Asp Asn Thr Leu Gln Gln Asn
 85 90 95
 Ser Ser Ser Asn Ile Ser Tyr Ser Asn Ala Met Gln Lys Glu Ile Thr
 100 105 110
 Leu Pro Ser Arg Leu Ile Tyr Tyr Ile Asn Gln Asp Ser Glu Ser Pro
 115 120 125
 Tyr His Val Leu Asp Thr Lys Ala Arg His Gln Gln Lys His Asn Lys
 130 135 140
 Ala Val His Leu Ala Gln Ala Ser Phe Gln Ile Glu Ala Phe Gly Ser
 145 150 155 160
 Lys Phe Ile Leu Asp Leu Ile Leu Asn Asn Gly Leu Leu Ser Ser Asp
 165 170 175
 Tyr Val Glu Ile His Tyr Glu Asn Gly Lys Pro Gln Tyr Ser Lys Gly
 180 185 190
 Gly Glu His Cys Tyr Tyr His Gly Ser Ile Arg Gly Val Lys Asp Ser
 195 200 205
 Lys Val Ala Leu Ser Thr Cys Asn Gly Leu His Gly Met Phe Glu Asp
 210 215 220
 Asp Thr Phe Val Tyr Met Ile Glu Pro Leu Glu Leu Val His Asp Glu
 225 230 235 240
 Lys Ser Thr Gly Arg Pro His Ile Ile Gln Lys Thr Leu Ala Gly Gln
 245 250 255
 Tyr Ser Lys Gln Met Lys Asn Leu Thr Met Glu Arg Gly Asp Gln Trp
 260 265 270
 Pro Phe Leu Ser Glu Leu Gln Trp Leu Lys Arg Arg Lys Arg Ala Val
 275 280 285
 Asn Pro Ser Arg Gly Ile Phe Glu Glu Met Lys Tyr Leu Glu Leu Met
 290 295 300
 Ile Val Asn Asp His Lys Thr Tyr Lys Lys His Arg Ser Ser His Ala
 305 310 315 320
 His Thr Asn Asn Phe Ala Lys Ser Val Val Asn Leu Val Asp Ser Ile
 325 330 335
 Tyr Lys Glu Gln Leu Asn Thr Arg Val Val Leu Val Ala Val Glu Thr
 340 345 350
 Trp Thr Glu Lys Asp Gln Ile Asp Ile Thr Thr Asn Pro Val Gln Met

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355	360	365
Leu His Glu Phe Ser Lys Tyr Arg Gln Arg Ile Lys Gln His Ala Asp		
370	375	380
Ala Val His Leu Ile Ser Arg Val Thr Phe His Tyr Lys Arg Ser Ser		
385	390	395
Leu Ser Tyr Phe Gly Gly Val Cys Ser Arg Thr Arg Gly Val Gly Val		
405	410	415
Asn Glu Tyr Gly Leu Pro Met Ala Val Ala Gln Val Leu Ser Gln Ser		
420	425	430
Leu Ala Gln Asn Leu Gly Ile Gln Trp Glu Pro Ser Ser Arg Lys Pro		
435	440	445
Lys Cys Asp Cys Thr Glu Ser Trp Gly Gly Cys Ile Met Glu Glu Thr		
450	455	460
Gly Val Ser His Ser Arg Lys Phe Ser Lys Cys Ser Ile Leu Glu Tyr		
465	470	475
Arg Asp Phe Leu Gln Arg Gly Gly Gly Ala Cys Leu Phe Asn Arg Pro		
485	490	495
Thr Lys Leu Phe Glu Pro Thr Glu Cys Gly Asn Gly Tyr Val Glu Ala		
500	505	510
Gly Glu Glu Cys Asp Cys Gly Phe His Val Glu Cys Tyr Gly Leu Cys		
515	520	525
Cys Lys Lys Cys Ser Leu Ser Asn Gly Ala His Cys Ser Asp Gly Pro		
530	535	540
Cys Cys Asn Asn Thr Ser Cys Leu Phe Gln Pro Arg Gly Tyr Glu Cys		
545	550	555
Arg Asp Ala Val Asn Glu Cys Asp Ile Thr Glu Tyr Cys Thr Gly Asp		
565	570	575
Ser Gly Gln Cys Pro Pro Asn Leu His Lys Gln Asp Gly Tyr Ala Cys		
580	585	590
Asn Gln Asn Gln Gly Arg Cys Tyr Asn Gly Glu Cys Lys Thr Arg Asp		
595	600	605
Asn Gln Cys Gln Tyr Ile Trp Gly Thr Lys Ala Ala Gly Ser Asp Lys		
610	615	620
Phe Cys Tyr Glu Lys Leu Asn Thr Glu Gly Thr Glu Lys Gly Asn Cys		
625	630	635
Gly Lys Asp Gly Asp Arg Trp Ile Gln Cys Ser Lys His Asp Val Phe		
645	650	655
Cys Gly Phe Leu Leu Cys Thr Asn Leu Thr Arg Ala Pro Arg Ile Gly		
660	665	670
Gln Leu Gln Gly Glu Ile Ile Pro Thr Ser Phe Tyr His Gln Gly Arg		
675	680	685
Val Ile Asp Cys Ser Gly Ala His Val Val Leu Asp Asp Thr Asp		
690	695	700

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Val Gly Tyr Val Glu Asp Gly Thr Pro Cys Gly Pro Ser Met Met Cys
 705 710 715 720
 Leu Asp Arg Lys Cys Leu Gln Ile Gln Ala Leu Asn Met Ser Ser Cys
 725 730 735
 Pro Leu Asp Ser Lys Gly Lys Val Cys Ser Gly His Gly Val Cys Ser
 740 745 750
 Asn Glu Ala Thr Cys Ile Cys Asp Phe Thr Trp Ala Gly Thr Asp Cys
 755 760 765
 Ser Ile Arg Asp Pro Val Arg Asn Leu His Pro Pro Lys Asp Glu Gly
 770 775 780
 Pro Lys Gly Pro Ser Ala Thr Asn Leu Ile Ile Gly Ser Ile Ala Gly
 785 790 795 800
 Ala Ile Leu Val Ala Ala Ile Val Leu Gly Gly Thr Gly Trp Gly Phe
 805 810 815
 Lys Asn Val Lys Lys Arg Arg Phe Asp Pro Thr Gln Gln Gly Pro Ile
 820 825 830

<210> 30
 <211> 37
 <212> DNA
 <213> Artificial/Unknown

<220>
 <223> primer

<400> 30
 ccggtcgacc accatggaac tccggaccgc aggctgg

37

<210> 31
 <211> 32
 <212> DNA
 <213> Artificial/Unknown

<220>
 <223> primer

<400> 31
 ccgaattctt accgccacct gggcctggct gc

32

<210> 32
 <211> 35
 <212> DNA
 <213> Artificial/Unknown

43/49

<220>

<223> primer

<400> 32

ccgctcgagc caccatgaag ccttttcata ctgcc

35

<210> 33

<211> 30

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 33

tccgaattct tattgtttgt aggtccgtgg

30

<210> 34

<211> 36

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 34

ccgctcgagc caccatgttg gctgcaaggc tgggtg

36

<210> 35

<211> 31

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 35

ccggatatct catttctttc tgttgccctcc a

31

<210> 36

<211> 34

<212> DNA

44/49

<213> Artificial/Unknown

<220>

<223> primer

<400> 36

ccgctcgagc caccatgagc acctcgtctg cgcg

34

<210> 37

<211> 29

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 37

tccgttaact taatagtcac catagttca

29

<210> 38

<211> 20

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 38

agctcattac tgtatattta

20

<210> 39

<211> 20

<212> DNA

<213> Artificial/Unknown

<220>

<223> primer

<400> 39

gctatatttc ataagtcac

20

<210> 40

<211> 26

45/49

<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 40
ctcgggaagc gcgccattgt gttggt

26

<210> 41
<211> 34
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 41
ccgctcgagc caccatgcgt tttgcctct tctc

34

<210> 42
<211> 28
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 42
cggaattctt attggttcac tctgtctg

28

<210> 43
<211> 33
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 43
acgcgtcgac ccaccatgcc ccgctacgag ttg

33

<210> 44

46/49

<211> 29
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 44
attgaattct cacttcttcc tctcttttg 29

<210> 45
<211> 35
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 45
ccgctcgagc caccatgaag ccgcccggca gcatc 35

<210> 46
<211> 29
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 46
cggaattctc agatggggcc ttgctgagt 29

<210> 47
<211> 1254
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (18)..(746)

<400> 47
ccgctcgagc cgcccag atg cag ttt cgc ctt ttc tcc ttt gcc ctc atc 50

47/49

Met Gln Phe Arg Leu Phe Ser Phe Ala Leu Ile																	
1						5						10					
att	ctg	aac	tgc	atg	gat	tac	agc	cac	tgc	caa	ggc	aac	cga	tgg	aga		98
Ile	Leu	Asn	Cys	Met	Asp	Tyr	Ser	His	Cys	Gln	Gly	Asn	Arg	Trp	Arg		
15						20						25					
cgc	agt	aag	cga	gct	agt	tat	gta	tca	aat	ccc	att	tgc	aag	ggg	tgt		146
Arg	Ser	Lys	Arg	Ala	Ser	Tyr	Val	Ser	Asn	Pro	Ile	Cys	Lys	Gly	Cys		
30						35						40					
ttg	tct	tgt	tca	aag	gac	aat	ggg	tgt	agc	cga	tgt	caa	cag	aag	ttg		194
Leu	Ser	Cys	Ser	Lys	Asp	Asn	Gly	Cys	Ser	Arg	Cys	Gln	Gln	Lys	Leu		
45						50						55					
ttc	ttc	ttc	ctt	cga	aga	gaa	ggg	atg	cgc	cag	tat	gga	gag	tgc	ctg		242
Phe	Phe	Phe	Leu	Arg	Arg	Glu	Gly	Met	Arg	Gln	Tyr	Gly	Glu	Cys	Leu		
60						65						70					
cat	tcc	tgc	cca	tcc	ggg	tac	tat	gga	cac	cga	gcc	cca	gat	atg	aac		290
His	Ser	Cys	Pro	Ser	Gly	Tyr	Tyr	Gly	His	Arg	Ala	Pro	Asp	Met	Asn		
80						85						90					
aga	tgt	gca	aga	tgc	aga	ata	gaa	aac	tgt	gat	tct	tgc	ttt	agc	aaa		338
Arg	Cys	Ala	Arg	Cys	Arg	Ile	Glu	Asn	Cys	Asp	Ser	Cys	Phe	Ser	Lys		
95						100						105					
gac	ttt	tgt	acc	aag	tgc	aaa	gta	ggc	ttt	tat	ttg	cat	aga	ggc	cgt		386
Asp	Phe	Cys	Thr	Lys	Cys	Lys	Val	Gly	Phe	Tyr	Leu	His	Arg	Gly	Arg		
110						115						120					
tgc	ttt	gat	gaa	tgt	cca	gat	ggg	ttt	gca	cca	tta	gaa	gaa	acc	atg		434
Cys	Phe	Asp	Glu	Cys	Pro	Asp	Gly	Phe	Ala	Pro	Leu	Glu	Glu	Thr	Met		
125						130						135					
gaa	tgt	gtg	gaa	gga	tgt	gaa	gtt	ggg	cat	tgg	agc	gaa	tgg	gga	act		482
Glu	Cys	Val	Glu	Gly	Cys	Glu	Val	Gly	His	Trp	Ser	Glu	Trp	Gly	Thr		
140						145						150					
tgt	agc	aga	aat	aat	cgc	aca	tgt	gga	ttt	aaa	tgg	ggg	ctg	gaa	acc		530
Cys	Ser	Arg	Asn	Asn	Arg	Thr	Cys	Gly	Phe	Lys	Trp	Gly	Leu	Glu	Thr		
160						165						170					
aga	aca	cgg	caa	att	gtt	aaa	aag	cca	gtg	aaa	gac	aca	ata	ctg	tgt		578
Arg	Thr	Arg	Gln	Ile	Val	Lys	Lys	Pro	Val	Lys	Asp	Thr	Ile	Leu	Cys		
175						180						185					
cca	acc	att	gct	gaa	tcc	agg	aga	tgc	aag	atg	aca	atg	agg	cat	tgt		626
Pro	Thr	Ile	Ala	Glu	Ser	Arg	Arg	Cys	Lys	Met	Thr	Met	Arg	His	Cys		
190						195						200					
cca	gga	ggg	aag	aga	aca	cca	aag	gcg	aag	gag	aag	agg	aac	aag	aaa		674
Pro	Gly	Gly	Lys	Arg	Thr	Pro	Lys	Ala	Lys	Glu	Lys	Arg	Asn	Lys	Lys		
205						210						215					
aag	aaa	agg	aag	ctg	ata	gaa	agg	gcc	cag	gag	caa	cac	agc	gtc	ttc		722
Lys	Lys	Arg	Lys	Leu	Ile	Glu	Arg	Ala	Gln	Glu	Gln	His	Ser	Val	Phe		

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220 225 230 235
 cta gct aca gac aga gct aac caa taaaacaaga gatccggtag atttttaggg 776
 Leu Ala Thr Asp Arg Ala Asn Gln
 240
 gtttttgttt ttgcaaatgt gcacaaagct actctccact cctgcacact ggtgtgcagc 836
 ctttgtgctg ctctgcccag tatctgttcc cagtaacatg gtgaaaggaa gcaccaccag 896
 catggccct gtgttattta tgctttgatt tgaatctgga gactgtgaag gcaggagtaa 956
 gtgcacagcc cgtgacttgg ctacagtgtg gctgagagaa tccgtccccg gcaccatgga 1016
 catgctagag gtgtgaggct gcagaacacc gctggaggac ggacttgtgc ctatttatgt 1076
 gaaagaagat gcttggcagg caatgcgcta ctactcgtg acctttatit ctcacattgt 1136
 gcattttcaa ggatatgttt gtgtggatat ctgcttagtg ttaccacatg gtattctcag 1196
 catgttacct tcacactgtt gtgcgatgaa actgcttita gctgaggata tgctctgg 1254

<210> 48
 <211> 243
 <212> PRT
 <213> Homo sapiens

<400> 48
 Met Gln Phe Arg Leu Phe Ser Phe Ala Leu Ile Ile Leu Asn Cys Met
 1 5 10 15
 Asp Tyr Ser His Cys Gln Gly Asn Arg Trp Arg Arg Ser Lys Arg Ala
 20 25 30
 Ser Tyr Val Ser Asn Pro Ile Cys Lys Gly Cys Leu Ser Cys Ser Lys
 35 40 45
 Asp Asn Gly Cys Ser Arg Cys Gln Gln Lys Leu Phe Phe Phe Leu Arg
 50 55 60
 Arg Glu Gly Met Arg Gln Tyr Gly Glu Cys Leu His Ser Cys Pro Ser
 65 70 75 80
 Gly Tyr Tyr Gly His Arg Ala Pro Asp Met Asn Arg Cys Ala Arg Cys
 85 90 95
 Arg Ile Glu Asn Cys Asp Ser Cys Phe Ser Lys Asp Phe Cys Thr Lys
 100 105 110
 Cys Lys Val Gly Phe Tyr Leu His Arg Gly Arg Cys Phe Asp Glu Cys
 115 120 125
 Pro Asp Gly Phe Ala Pro Leu Glu Glu Thr Met Glu Cys Val Glu Gly
 130 135 140
 Cys Glu Val Gly His Trp Ser Glu Trp Gly Thr Cys Ser Arg Asn Asn
 145 150 155 160
 Arg Thr Cys Gly Phe Lys Trp Gly Leu Glu Thr Arg Thr Arg Gln Ile
 165 170 175
 Val Lys Lys Pro Val Lys Asp Thr Ile Leu Cys Pro Thr Ile Ala Glu
 180 185 190

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Ser Arg Arg Cys Lys Met Thr Met Arg His Cys Pro Gly Gly Lys Arg
195 200 205
Thr Pro Lys Ala Lys Glu Lys Arg Asn Lys Lys Lys Lys Arg Lys Leu
210 215 220
Ile Glu Arg Ala Gln Glu Gln His Ser Val Phe Leu Ala Thr Asp Arg
225 230 235 240
Ala Asn Gln

<210> 49
<211> 29
<212> DNA
<213> Artificial/Unknown

<220>
<223> primer

<400> 49
ccgctcgagc cgcccagatg cagtttcgc